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OW nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:37:52 ; Search time 2932.86 Seconds
(without alignments)
5458.535 Million cell updates/sec

Title: US-09-601-138-1

Perfect score: 1035
Sequence: 1 atgagagtgatcgctggtgg.....aattgacgatgcccatata 1035

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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97: gb_pi13:*
98: em_ba3:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1035	100.0	9 AX020182	AX020182 Sequence
2	1035	100.0	10 AX079027	AX079027 Sequence
3	1035	100.0	9 AX020193	AX020193 Sequence
4	1035	100.0	10 AX079028	AX079028 Sequence
5	1035	100.0	9 AX020191	AX020191 Sequence
6	1035	100.0	10 AX079037	AX079037 Sequence
7	1035	100.0	9 AX020190	AX020190 Sequence
8	1035	100.0	10 AX079036	AX079036 Sequence

9	1033.4	99.8	1035	9	AX020183	AX020183 Sequence
10	1033.4	99.8	1035	9	AX020184	AX020184 Sequence
11	1033.4	99.8	1035	10	AX079029	AX079029 Sequence
12	1033.4	99.8	1035	10	AX079030	AX079030 Sequence
13	1031.8	99.7	1035	9	AX020187	AX020187 Sequence
14	1031.8	99.7	1035	10	AX079033	AX079033 Sequence
15	1030.2	99.5	1035	9	AX020189	AX020189 Sequence
16	1030.2	99.5	1035	10	AX079035	AX079035 Sequence
17	1030.2	99.5	1035	9	AX020192	AX020192 Sequence
18	1030.2	99.5	1035	10	AX079025	AX079025 Sequence
19	1028.6	99.4	1035	9	AX020186	AX020186 Sequence
20	1028.6	99.4	1035	10	AX079032	AX079032 Sequence
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23	1025.4	98.7	1377	93	HSPBDR2	HSPBDR2 Homo sapi
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27	1021.4	98.7	1034	10	AX079034	AX079034 Sequence
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32	236.2	22.8	122349	2	D90908	D90908 Synecocyst
33	176.8	17.1	9958	1	AE004938	AE004938 Pseudomon
34	172.2	16.6	10024	97	HOMEBGDA	HOMEBGDA Homo sapien
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36	172.2	16.6	144794	82	AP001182	AP001182 Homo sapi
37	172.2	16.6	157405	82	AP001315	AP001315 Homo sapi
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39	172.2	16.6	196511	82	AP000854	AP000854 Homo sapi
40	166.2	15.1	6301	1	AF064061	AF064061 Pseudobact
41	162.2	15.7	294250	2	AP001517	AP001517 Bacillus
42	162	15.7	110000	84	LMFICHR2_24	LMFICHR2_24 Cont.uation (25 o
43	161	15.6	5852	2	AF221100	AF221100 Selenomon
44	160.6	15.5	269223	10	AX067466	AX067466 Sequence
45	159	15.4	1872	3	PSEHEMCD	PSEHEMCD Pseudomonas

ALIGNMENTS

RESULT 1						
LOCUS	AX020182	1035 bp	DNA	PAT	07-SEP-2000	
DEFINITION	Sequence 1 from Patent WO937325.					
ACCESSION	AX020182					
VERSION	AX020182.1	GI:10043973				
KEYWORDS						
SOURCE	unidentified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 1035)					
AUTHORS	Fogh, J. and Gallier, P.					
TITLE	Method for treating acute intermittent porphyria (aip) and other					
JOURNAL	Patent: WO 93/7325-A/1 29-JUL-1999;					
FOOTNOTES	1-1035					
FEATURES	source					
BASE COUNT	250 a 271 c 302 g 212 t					
ORIGIN	/organism="unidentified"					
	/db_xref="taxon:32644"					

Query Match 100.0%; Score 1035; DB 9; Length 1035;
Best Local Similarity 100.0%; Pred. No. 4, 5e-238;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 atgagagtgatctcgcgtggtgtaaccgaagacagcgtctgctgcaaacagacgacgt 60
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QY	121	accacagggagacaagatctctgtatctgacatcttaagatttgagagaaagcctgtt 180
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QY	181	accagaagatctgaaacatgacctggtgagaaatgaaagtgaacctgtgttcacatcc 240
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QY	421	ttccggaatctgagttcagaggtatctggggaaacctcaaccccgctctggaagctg 480
Db	421	ttccggaatctgagttcagaggtatctggggaaacctcaaccccgctctggaagctg 480
QY	481	gagcagcagcagagatctcagtcacatccctggtgaaacagctgtgctcagcagcagtg 540
Db	481	gagcagcagcagagatctcagtcacatccctggtgaaacagctgtgctcagcagcagtg 540
QY	541	tggcacaacacaggtgtggcagaacctcgtcagccctgagaaatgagatgtgtgtggccag 600
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Db	1021	aagcagtgcccaataa 1035

RESULT 2
LOCUS AX079027 1035 bp DNA PAT 22-FEB-2001

DEFINITION	Sequence 3 from Patent WO0107065.
ACCESSION	AX079027
VERSION	AX079027.1
KEYWORDS	GI:13158602
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1. (bases 1 to 1035)
TITLE	Gellerfors, P. and Poch, J.
JOURNAL	Production of rhbpgd and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyric diseases
FEATURES	Patent: WO 0107065-A 3 01-FEB-2001; Hemelotech A/S (DK)
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	/db_xref="taxon:9606"
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	Best Local Similarity	100.0%	Pred. No. 4, 5e-238;		
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				Indels	0;
				Gaps	0
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Db	1	ATGGAAGATGATTGGCGTGGGTACCCCAAGACCGACTTGCATCAGACCGAGAGT	60		
OY	61	gtgtgtgcaacattgaaagcctcgtaacccctggccgcagcttgaaatcattgcatctc	120		
Db	61	GTGTGGCAACATTGAAAGCGCTGTACCTGGCGCTGCAATTGAAATCATTTGCTATGCC	120		
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Db	121	ACCAAGAGGACACAAGATTCTTGATACTGTGACCTCTAAATATGGAGAAAGCGCTGTT	180		
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Db	181	ACCAAGAGCGCTTGAAACATATGCCCTGAGAAAGAAATGAAGTGAACCTGGTTGCTACCTCTG	240		
OY	241	aaggaactgcgccactgctgctctcctctgcttcacacatgagagccattctgaacgggaa	300		
Db	241	AAGGAACCTGCCACTGTGCTCTCTCTGCTTCACCATCGAGCCATCTGGAACCGGAA	300		
OY	301	aacctcatgatgctgtgtcttcttcacccaataattgttggaaagacctaagaaacctg	360		
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OY	361	ccgaagaagaagtgtygtgggaaccagcttcccctgagaaagagagccagctgcagaagaag	420		
Db	361	CGAGGAAGAGTGTGGTGGGAAACCACTCCCTGCGAAGAGCAGCCCACTCCAGAGAAAG	420		
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Db	481	GACAGACGACGAGAGTTCAATGCACTCATCTCTCTGCAACAGCTGGCGCTCAAGCGATGGGC	540		
OY	541	tggacacaacccggtctgggcagatcctctcaacccttgaaatgtgatgtatgctgtggccag	600		
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Db	601	GGGGCCTTGGGCGTGGAGTGCAGGCCAAGACCAAGAGACATCTTGGATCTGCTGGGCTG	660		
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[illegible]

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DEFINITION	Sequence 12 from Patent WO9937325.				
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VERSION	AX020193.1 GI:10043984				
KEYWORDS					
SOURCE	unidentified.				
ORGANISM	unidentified				
REFERENCE	1 (bases 1 to 1113)				
AUTHORS	Fogh, J. and Gellerfors, P.				
TITLE	Method for treating acute intermittent porphyria (a1p) and other porphyric diseases				
JOURNAL	Patent: WO 9937325-A 12-29-JUL-1999;				
FEATURES	POGH JENS (DK); HEMMELOECH A S (DK); GELLERFORS PAER (SE)				
SOURCE	Location/Qualifiers				
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Best Local Similarity	100.0%; Pred. No. 4, 5e-238;				
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Oy	61	gtgctggtgcaacattgtaaaagcctcgtaaccctgcgcgcagcttggaaatcatgtatgtcc	120		
Db	139	gtgtgtgcaacattgtaaaagcctcgtaaccctgcgcgcagcttggaaatcatgtatgtcc	198		
Oy	121	accacagggagacaagatctctgtatctgtaactctctaagatttgagagaaagcgtttt	180		
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Oy	181	accagaagacttgaacatgccctcggaagaagaatgaagtggacccgtgttctactccttg	240		
Db	239	accagaagacttgaacatgccctcggaagaagaatgaagtggacccgtgttctactccttg	318		
Oy	241	aagagctgcccaactgtgtcttcctcgtgtctaccacatcggaagcactctggaacgagaa	300		

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Qy 421 TCCCGCATCTGAGTTCAGAGACTATTGGGAAACCTCAACACCCGCTTCCGAACTG 558
Db 499 TTCCCGCATCTGAGTTCAGAGACTATTGGGAAACCTCAACACCCGCTTCCGAACTG 558
Qy 481 GAGAGAGAGAGAGTTCAGTCCATCATCTGCAAGAGCAAGCTGCTGCAAGAGAGAG 540
Db 559 GAGAGAGAGAGAGTTCAGTCCATCATCTGCAAGAGCAAGCTGCTGCAAGAGAGAG 618
Qy 541 TGGCAAAACCGGGTTGGCAGATCCGCAACCTTGAGAAATCTGATGCTGTGGGCTG 678
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Qy 961 CTGACAGATCCGAGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
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Qy 1021 AACCTCATGCTGTCTGTCTCTTCCACCAAAATTTGTTGGAAACCTTGAAACCTTG 1035
Db 1099 AACCTCATGCTGTCTGTCTCTTCCACCAAAATTTGTTGGAAACCTTGAAACCTTG 1113

RESULT 4
AX079028 1113 bp DNA PAT 22-FEB-2001
LOCUS AX079028
DEFINITION Sequence 4 from Patent WO0107065.
ACCESSION AX079028
VERSION AX079028.1 GI:13158603
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1113)
AUTHORS Gellera, P., and Fogh, J.
TITLE Production of rmpbd and new therapeutic methods for treating
porphyric diseases
JOURNAL Patent: WO 0107065-A 4 01-FEB-2001;
Hembiotech A/S (DK)

FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
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ORIGIN
Query Match 100.0%; Score 1035; DB 10; Length 1113;
Best Local Similarity 100.0%; Pred. No. 4.5e-238;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 79 ATGAGAGTATGCTGT 138
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Db 139 GT 198
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RESULT 5
AX020191 1260 bp DNA PAT 07-SEP-2000
LOCUS Sequence 10 from Patent WO937325.
ACCESSION AX020191
VERSION AX020191.1 GI:10043982
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Fogh,J. and Gellerfors,P.
TITLE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 937325-A 10 29-JUL-1999;
FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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REFERENCE 1 (bases 1 to 1260)
AUTHORS Gellerfors,P. and Fogh,J.
TITLE Production of htpgd and new therapeutic methods for treating
patients with acute intermittent porphyria (aip) and other
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TITLE		Method for treating acute intermittent porphyria (aip) and other porphyric diseases				
JOURNAL		Patent: WO 9937325-A 9 29-JUL-1999;				
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REFERENCE	1. (bases 1 to 3988) Gellerfors, P. and Fogh, J. Production of rmpgd and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyritic diseases Patent: WO 0107065-A 12 01-FEB-2001;		
JOURNAL	Hembiotech A/S (DK)		
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VERSION AX020184.1 GI:10043975
KEYWORDS
SOURCE
ORGANISM unidentified.
unclassified.
1 (bases 1 to 1035)
REFERENCE
Fogh,J. and Gellerafors,P.
TITLE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 937325-A 3 29-JUL-1999;
FOGH JENS (DK); HEMBIOTEC A S (DK); GELLERFORS PAER (SE)
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE	1 (bases 1 to 1035)	
JOURNAL	Gellerfors, P., and Fogh, J. Production of rhpbpd and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyric diseases Patent: WO 0107065-A 6 01-FEB-2001; Hemebiotech A/S (DK)	
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AUTHORS	1 (bases 1 to 1035)		
TITLE	Fogh,J. and Gellerfors,P.		
JOURNAL	Method for treating acute intermittent porphyria (aip) and other porphyric diseases		
FEATURES	Patent: WO 937325-A 6 29-JUL-1999;		
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 REFERENCE 1 (bases 1 to 1035)
 AUTHORS Gellerfors, P. and Fogh, J.
 TITLE Production of rmpgd and new therapeutic methods for treating
 porphyria with acute intermittent porphyria (aip) and other
 Patent: WO 0107065-A 9 01-FEB-2001;
 JOURNAL HemeBioTech A/S (DK)
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REFERENCE 1 (bases 1 to 1035)
AUTHORS Fogh, J. and Gellerfors, P.
TITLE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 93/7325-A 8-29-JUL-1999;
FOGH JENS (DK); HEMEBIOTECH A S (DK); GELLERFORS PAER (SE)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

QY 835 caggctaccatcactctcctcctgacagca tgaagatgccccggagatgaccccaactg 894
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 Db 660 CAGGCTACATCCATGCTGCTCCTGCCGACATGAGATGGCCGAGGATGACCCACACTTG 719
 QY 895 gtaagctcactctgctgtaacatctcaagagggcccaagcttgctgctccaggaactggc 954
 |||
 Db 720 GTAGGCACTACTGCTGTAACATCCACGAGGCCCCGACTGTGCTGCCAGCACTTGCGG 779
 QY 955 atcagctggcccaactctgtctgtagcaagagagccaaacacatccctggatgtgtgacgg 1014
 |||
 Db 780 ATCAGCCTGGCCAACTGTTGCTGAGACAAAGACGCAAAACATCTGATGTTTGACGG 839
 QY 1015 caattgaagagatcccatc 1033
 |||
 Db 840 CAGCTTAAGATGCCCAATT 858

RESULT 2
 AL520285 1036 bp mRNA EST 13-FEB-2001
 LOCUS AL520285 LTI_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006Y607 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL520285
 VERSION AL520285.1 GI:12783778
 KEIWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1036)
 AUTHORS Li, W.-B., Gruber, C., Jessse, J. and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 1. 1036

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DB006Y607"
 /clone_1id="LTI_NFL004_NBC2"
 /sex="male"
 /tissue-type="neuroblastoma cells"
 /lab_host="DH10b"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : filangel@life.com URL : http://fulllength.invitrogen.com" 1 others

BASE COUNT 243 a 262 c 310 g 200 t

Query Match 77.8% Score 804.8 DB 105 Length 1036
 Best Local Similarity 99.1% Pred. No. 1.8e-204
 Matches 850; Conservative 1; Mismatches 3; Indels 4; Gaps 4;

QY 1 atgagagcgatcgcgctgtagccgcgaagagccagctgctgcgtacacagcgagcagt 60
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 Db 179 ATGAGAGCGATTCCTGGCTGGTACCCGGAAGAGCCACTTGGCTGCTACAGACGACAGT 238
 QY 61 gtgtgtgcaacatctgaagcctcgtaaccctgacctgcaatcttgaaatcaatctctatgtcc 120
 |||
 Db 239 GTGTGTGCAACATTCGAAGCCTCGTACCTGGCTGCAAGTGAATCATCTCTATGTGCC 298

QY 121 acccaaggagacaagaattcttgatactgcaactctctaagatctggaagaaagcccttct 180
 |||
 Db 299 ACCCAGAGGACAAAGATTCTTGATACCTGACTCTCTAAGATGTGAGAAAGCCCTGTT 358
 QY 181 accaagagccttgaaatagcccttggaagaagatgaatggaacctggtgtctcaactctg 240
 |||
 Db 359 ACCAAGAGCTTTAAACATCTCCCTTGAGAAAGATGAAGGACCTGGTTGTTCACTCTCTTG 418
 QY 241 aaggaactgcceactgtgtctctcctcctgcttcacacatcgagagcaatctgaaagcggaa 300
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 Db 419 AAGGACCTGCCCACTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478
 QY 301 aaccctcatgactgtgtgtctcttcaacaaatcttggaagagccctggaagacccg 360
 |||
 Db 479 AACCTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 538
 QY 361 ccaagaagaagatgtgtgtgtggaacagctccctcgaaagagcagccagctgacagagaag 420
 |||
 Db 539 CCAAGAGAAGATGTGTGTGGAAACAGCTCCCTCGGAAGACAGCCAGCTGCAGAGAAAG 598
 QY 421 ctccgcactctgagctcaagagatctcgagggaacacacacccggcttcggaagctg 480
 |||
 Db 599 TTCCCGCATCTGAGATTCAGAGATTCGAGATTCGAGATTCGAGATTCGAGATTCGAGATTC 658
 QY 481 gaagagcagcagaagatctgaatgcatcactctggaacagctgagccctgcaagctgagc 540
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 Db 659 GACGACACACAGAGATTCAGTCCATCTCTGCAACAGCTGCTGCAAGGCAATGGGC 718
 QY 541 tggacaacacgggtgtggacagatctccgacacccctggaagaaagcatgtatctgtggcag 600
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 Db 719 TGGCAACACCGGCTGGGCAATCTCTGCAACAGCTGCTGCAACAGCTGCTGCAACAGCTG 778
 QY 601 gaggcccttgaggctggaagctgcgaagcgaagagacacacacacacacacacacacacac 660
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 Db 779 GGGGCTTGGGCTGGAAGTCCGAGTCCGAGCCAGACAGACAGACAGACAGACAGACAGACAG 838
 QY 661 ctgcagcagctccggaagctctgctcctgctgcaatgctggaagggcctcttcagagcctg 720
 |||
 Db 839 CTGCAGATCCCGACACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 897
 QY 721 gaaggagctgtagctgtagctgtagctgtagctgtagctgtagctgtagctgtagctgtag 780
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 Db 898 GAAGGAGGCTGAGTGTCCAGTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 957
 QY 781 ctgactggaagagctctggaagctgtagctgtagctgtagctgtagctgtagctgtagctg 840
 |||
 Db 958 CTGACTGAGAGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAG 1015
 QY 841 accatccatgtccctgccc 858
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 Db 1016 A-CATCCATGTCCCGGCC 1032

RESULT 3
 BG337601 904 bp mRNA EST 27-FEB-2001
 LOCUS 602435148F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:455315 5'
 DEFINITION mRNA sequence.
 ACCESSION BG337601
 VERSION BG337601.1 GI:13144039
 KEIWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 904)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: gtraps@email.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rudin Laboratory

LOCUS AL557370 942 bp mRNA EST 16-FEB-2001
DEFINITION AL557370 LRL_FL012_Tc1 Homo sapiens cDNA clone CS0DH004Yp13 5 prime
ACCESSION AL557370
VERSION AL557370.1 GI:12900909
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 942)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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1. 942
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DH004Yp13"
/clone_1lb="LRL_FL012_Tc1"
/tissue_type="T cells from T cell leukemia"
/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 216 a 258 c 284 g 183 t 1 others
ORIGIN

Query Match 66.7%; Score 690.4; DB 106; Length 942;
Best Local Similarity 98.4%; Pred. No. 7e-174;
Matches 728; Conservative 1; Mismatches 7; Indels 4; Gaps 3;

OY 1 atgagagtgatcgcgtggtggtacccgcaagagccagcttgctgcatacagagcagcagt 60
DB 191 ATGAGAGTGAATTCGCGTGGGTACCCCAAGACCGCTTGCATGACAGACGACAGT 250
OY 61 gtggtgcaacatgaaagccctgctacccctgcccagcttggaatcatgtctgctc 120
DB 251 GTGGTGCACATGAAAGCTGTGACCTGGCGCTGCAGTTGAAATCATTTGCTATGCTC 310
OY 121 accacaggggaacagattctgatactgactctcttaagattgagagaaaagcctgtt 180
DB 311 ACCACAGGGGACAGATTCTTGATCTGACACTCTAGATTGAGAGAAAAAGCTGTTT 370
OY 181 accaagagcttgaacaatgcccctgagagaagaatgagaccttggttctactccttg 240
DB 371 ACCAAGAGCTTGAACATGCGCTGGAGAAATGAAGTGGACCTGTTGTTCTACTCTTC 430
OY 241 aagaactgcccacactgtctctcctctgctcagcttcacatcagacatctgcaacgagaa 300
DB 431 AAGGACTCTGCCACTGTGCTTCTCTCTGCTTCACCATCGAGGCATCTGCACACGGGAA 490
OY 301 aacctcatgatgctgtgtctcttccaccaaaattgttggagaagaccctagaacccctg 360
DB 491 AACCTCATGATGCTGTGTCTTTCACCCAAATTTGTTGGAGAACCTTGAAACCTTG 550
OY 361 ccagagaagagtggtggtggaacagctccctcgtcgaagagcaccagctgcagagaag 420
DB 551 CCAGAGAAGAGTGTGTGTGGGAACACAGCTCCCTGCGAAGAGCAGCCCACTCAGAGAAG 610
OY 421 ttcccgatctcgagattcagagattctcggggaaccccaacacccgcttcgagaacgtg 480

DB 611 TTCCCGCATGTGAGTTTCAGAGACTATTCGGGAAACCTCAACACCCGGCTTCGAAAGCTG 670
OY 481 gacgagcagcaggaagcttcagctgcccacatcctctggaacagcctgcccagcagcagtg 99 539
DB 671 GACGAGCAGCAGAGTTCAAGTGCATCATCTGCGAACACAGCTGCGACGCCATGTGG 720
OY 540 ctggcacaacccgggtggcagatctctgacacccctgaagatgcatgatactgtagggcca 599
DB 731 CTGGCACAAACCCGGGTGGGAGATCTCTGCACCCCTGAGAAATGCAFTGATGCTGAGGCCA 790
OY 600 gggggccttgggcgtggaagtgcgagcgaagcagagacatcttgatctggtggtggt 659
DB 791 GGGGG-CTTGGGGGTGGAAGTGGACCAAGCAGCAGGACATCTTGATCTGTGGGTGT 849
OY 660 gctgacgacatcccgagacatctgctctgctgcatgctgaaagggccttcgaagccct 719
DB 850 GCTCAGCATCCCGAGACATCTGCTTGCATGATCCGTGAAGGGCTTCCGAG--CACC 907
OY 720 ggaagagagctgcagtgctgc 739
DB 908 TGAAGAGAGCTCGAGTGTGC 927

RESULT 7
AL579416/c 838 bp mRNA EST 16-FEB-2001
LOCUS AL579416 LRL_FL012_Tc1 Homo sapiens cDNA clone CS0DH004Yp13 3 prime
DEFINITION AL579416 LRL_FL012_Tc1 Homo sapiens cDNA clone CS0DH004Yp13 3 prime
ACCESSION AL579416
VERSION AL579416.1 GI:12944439
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 838)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
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1. 838
/organism="Homo sapiens"
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/clone="CS0DH004Yp13"
/clone_1lb="LRL_FL012_Tc1"
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/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 160 a 243 c 225 g 189 t 21 others
ORIGIN

Query Match 65.9%; Score 682; DB 106; Length 838;
Best Local Similarity 95.4%; Pred. No. 1.2e-171;
Matches 702; Conservative 18; Mismatches 14; Indels 2; Gaps 2;

OY 300 aaacctcatgatgctgtgtcttctcaaccaaatgttggagaagaccctagaacccct 359
DB 838 AACCTCATGATGCTGTGTCTTTCACCCAAATTTGTTGGAGAACCTTGAAACCTT 780
OY 360 gccagagaagagtggtggtggaacccgctccctctgagagaagagcaccagctgcagagaaa 419

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Db 779 GCCAGAGAAAGAGTGTGGGAACCACTCCCTCCGACAGACGCCAGCTGCAGAGAAA 720
Oy 420 GTCCGCAATCTGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 479
Db 719 GTTCCCGATCTGAGATTCAGAGATATTCGGGAAACCTCAACACCCGCTTCGGAAGCT 660
Oy 480 GAGCAGAGAGAGAGTTCAGTGCATCATCTCGGACACAGCTGGCCCTGCAGCCATGCG 539
Db 659 GACACAGCAGCAGAGATTCAGTGCATCATCTCGGACACAGCTGGCCCTGCAGCCATGCG 600
Oy 540 CTGGCAACAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 599
Db 599 CTGGCAACAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 540
Oy 600 GAGGAGCTGAGGATTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 559
Db 539 GAGGAGCTGAGGATTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 480
Oy 660 GCTGCAACAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 719
Db 479 GCTGCAACAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 421
Oy 720 GAGGAGAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 779
Db 420 GAGGAGAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 361
Oy 780 CCTGCAACAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 839
Db 360 CCTGCAACAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 301
Oy 840 TACCATCAGTTCCTCCGACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 899
Db 300 TACCATCAGTTCCTCCGACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241
Oy 900 CACCACTGCTGTAACATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959
Db 240 CACCACTGCTGTAACATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 181
Oy 960 CCTGCAACAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 1019
Db 180 CCTGCAACAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 121
Oy 1020 GAGGAGAGAGTTCGAGGATCTCGGGAAACCTCAACACCCGCTTCGGAAGCT 121
Db 120 TACCATCAGTTCCTCCGACAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG

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RESULT 8
LOCUS BE547860 804 bp mRNA EST 09-AUG-2000
DEFINITION Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
ACCESSION BE547860
VERSION BE547860.1 GI:9776505
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 804)
NIH-MGC http://mgi.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

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FEATURES
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            /lab_host="DH10B"
            /note="Organ: cervix; Vector: pCMV-Sport6; Site_1: Not;
            Site_2: Salt; Cloned unidirectionally. Primer: Oligo dt.
            Average insert size 1.4 kb. Library prepared by Life
            Technologies."
BASE COUNT 171 a 226 c 235 g 172 t
ORIGIN
Query Match 64.9% Score 671.4; DB 137; Length 804;
Best Local Similarity 94.0% Pred. No. 8.1e-169;
Matches 742; Conservative 0; Mismatches 41; Indels 6; Gaps 4;
Oy 8 Tgattcggctgggtaccggaagagcagctgtctgcatacagaagagatgtgtgtg 67
Db 1 Tgattcggctgggtaccggaagagcagctgtctgcatacagaagagatgtgtgtg 60
Oy 68 caaatgtgaagcctgtacccctgtgacccctgtgacccctgtgacccctgtgaccc 127
Db 61 CAACATTGAAAGCCTGTGACCTGCTGACCTGCTGACCTGCTGACCTGCTGACCTG 120
Oy 128 ggaagaagatctctgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 187
Db 121 GGCAGCAAGATTCTGTATGACTGACCTGACCTGACCTGACCTGACCTGACCTG 180
Oy 188 agcttaaacatgacctgtgaagaaatgaatgaatgaatgaatgaatgaatgaatga 247
Db 181 AGCTTAAACATCCCTGGAAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
Oy 248 tggcacaatgtctctctctctctctctctctctctctctctctctctctctct 307
Db 241 TGCCCACTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Oy 308 atgagctgtgtctctctctctctctctctctctctctctctctctctctctct 367
Db 301 ATGATGCTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
Oy 368 agagtgatgtggaagacagcctcctgtggaagacagcctcctgtggaagacagc 427
Db 361 AGAGTGTGTGTGGAACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Oy 428 atctggaatctggaatctggaatctggaatctggaatctggaatctggaatctgga 487
Db 421 ATCTGAGTTCAGAGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Oy 488 agcaagagatcagtgacatcctctgtgcaagacagctgtgcaagacagctgtgca 547
Db 481 AGCAGAGATTCAGTGCATCTCTGCAACACCTGCTGCAACACCTGCTGCAACAC 540
Oy 548 accgggtctggaagatctgtggaatctggaatctggaatctggaatctggaatctgga 607
Db 541 ACCGGGTGAGGAGATCTGTGCAACACCTGCTGCAACACCTGCTGCAACACCTG 600
Oy 608 tgggctgtggaagatctgtggaatctggaatctggaatctggaatctggaatctgga 667
Db 601 TGGGCTGTGGAAGATCTGTGCAACACCTGCTGCAACACCTGCTGCAACACCTG 660
Oy 668 atcccgagactgtcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 723
Db 661 ATCCGAGACTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 720
Oy 724 -ggaagtgagtgatgagcagtgacatcagcagcagcagcagcagcagcagcagcag 781
Db 721 CGGATGCTGCTTGTGCTGCTTGTGCTGCTTGTGCTGCTTGTGCTGCTTGTGCTG 780

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QY 782 tgactgag 790
Db 781 TGTGGCAG 789

RESULT 9
AL520284/c
LOCUS
DEFINITION AL520284 L1_NFL004_MBC2 Homo sapiens cDNA clone CS0DB0061607 3
ACCESSION AL520284 919 bp mRNA EST 13-FEB-2001
VERSION AL520284 prime, mRNA sequence.
KEYWORDS AL520284.1 GI:12783777
SOURCE EST.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 919)
AUTHORS Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
Source
1. 919
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CS0DB0061607"
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/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 191 a 276 c 248 g 202 t 2 others
ORIGIN

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Query Match 63.7%; Score 659.2; DB 105; Length 919;
Best Local Similarity 98.7%; Pred. No. 1.5e-165;
Matches 705; Conservative 1; Mismatches 4; Indels 4; Gaps 4;

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QY 322 ttccaccacaatttctgttggaagaccctgacagagaagatgtgtgga 381
Db 918 YTTACCCCAAAATTGTT-GGAAGACCTTAGAAACCTCCAGAGAGAGTGTGT-GCA 861
QY 382 accagctccctggcgaagagcagccagctggcagagaagtcccgcatctggatccagg 441
Db 860 ACCAGCTCCCTGGCAAGAGCAAGCCAGCTGCAGAGAAAGTTCGCCATCTGGAGTTCAAG 801
QY 442 agtatctggggaacactcaaacaccgagcttcggaagcttgagagcagcagagattcagt 501
Db 800 AGTATTC-GGGAAACCTCAACACCCGGCTTCGAAAGCTGAGACGACGACAGAGATTCAAGT 742
QY 502 gccatcacctggagaagagctggctggcagcagcagatgtgtgcacaaacggattggagag 561
Db 741 GGCATCACTCTGGCAACAGCTGGCTGTCAGCGCATGGCTGGCAACCGGGTGGGGGAG 682
QY 562 atccctgacccctggagaatgcatgtatgtctgtgtggccagggggcttggcgttggaagt 621
Db 681 ATCTGCAACCTCGAGGAATCATGTATGTGTGTGGCCAGGCGGCTTGGCGCTGGAAAGTG 622

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QY 622 cgaagcgaagaccagagacatcttggaatctgggtgtgtgtgcagacatcccggaactctg 681
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QY 682 ctgcgtgcatcgtctgaagaaggccttcctgaagcaccctggaaagagcctgcagtgatgca 741
Db 562 CTTCGCTGCATCTCGCTGAAGAGGCGCTTCGTGAGGCAACCTTGAAAGAGCGCTGCAGTGTGCA 503
QY 742 gtagcgtgcatgaagctatgaagatgggcaactgtacactgtacctgcggaagagcttgagt 801
Db 502 GTAGCGGTGCTATACAGCTATGAGAGGATGGCAACTGTACCTTACGTGAGGAGTGTGAGT 443
QY 802 ctgaagcgtcagataagacatacaagagacacatgcaagcctacacatcgtccctggccag 861
Db 442 CTAGACGCTCAGATFACATACAAAGAGACCATGACAGGCTACATCATGTCCCTGCCAG 383
QY 862 catgaagatgtgcctctgtgagatgacccaagctgtgtgtagcatcaactgtctgaatcca 921
Db 382 CATGAAGATGGCCCTGTGAGATGACCCACAGATTGTGATGATCATCTGCTGATACATTCGA 323
QY 922 cgaagccccagctgtgctgcccagaacttgggcatcagccttggccaacttltgtgagc 981
Db 322 CGAGGGCCCGCAGTGTGGCTGGCCAGAACTTGGGATAGCGCTGCGCAACTTGTGTGAGC 263
QY 982 aaagagcccaaaaacatccctggaatgtgtgcagcgcaatggaacgatgccattaa 1035
Db 262 AAAGAGCCCAAAAACATCTGATGTTGCACGCGACCTTACGATGAGATGCCATTAA 209

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RESULT 10
BF035760 801 bp mRNA EST 20-OCT-2000
LOCUS 601458755F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862453 5',
DEFINITION mRNA sequence.
ACCESSION BF035760
VERSION BF035760.1 GI:10743500
KEYWORDS EST.
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 801)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DRP

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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LMA9600 row: m column: 14
High quality sequence stop: 678.

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/note="Organ: ovary; Vector: pCMV-Sport6; Site:1: NotI;
Site:2: SalI; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

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BASE COUNT 192 a 212 c 241 g 156 t
ORIGIN
Query Match 62.8%; Score 650.4; DB 143; Length 801;

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QY 660 gctgcacgacatccgagacatctgttcgtcgcacatcgtaagaagggccttcctgaagacacct 719
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Db 694 gctgcacgacatccgagacatctgttcgtcgcacatcgtaagaagggccttcctgaagacacct 753
QY 720 ggaagga-ggctgcagctgtgcagtagccgctg 750
|||||
Db 754 ggaaggaagggctgtgcagtagctgcagtagccgctg 785

RESULT 12
Bg469642 835 bp mRNA EST 21-MAR-2001
LOCUS 602533692F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661422 5',
DEFINITION mRNA sequence.
ACCESSION Bg469642
VERSION Bg469642.1 GI:13401917
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 835)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9apbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM1460 row: g column: 23
High quality sequence stop: 824.
Location/Qualifiers
1. 835
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/tissue_type="adenoecarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the Laboratory of Gerald W. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
BASE COUNT 194 a 229 c 250 g 162 t
ORIGIN

Query Match 62.5%; Score 646.4; DB 154; Length 835;
Best Local Similarity 99.6%; Pred. No. 4e-162;
Matches 669; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Db 163 atgagagtgatcgcgtgggtacccggaagagcagctgtcgcacacagcagcagc 222
QY 61 gtagggagacatggaagcctgtaaccggcctgagcttgaataatgctatgccc 120
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Db 223 gtagggagacatggaagcctgtaaccggcctgagcttgaataatgctatgccc 282
QY 121 accaagagggaagacatctgtatctacacacacacacacacacacacacacac 180
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Db 283 accaagagggaagacatctgtatctacacacacacacacacacacacacacac 342
QY 181 accaagaggcctggaacatgcctcgaggaagaatgaagtgtgacctgtgttacc 240

Db 343 ACCAGAGAGCTTGAAACATGCCCTGGAGAGAAAGATGAGACTGCTGTTGCTACCTCTG 402
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QY 241 aagagacatccac 300
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Db 403 AAGACGCTGCCACCTGCTGCTTCTCCTGCTTACCATGAGCATCTGCAACGGGAA 462
QY 301 aacctatgactgt 360
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Db 463 AACCTCATGATGCTGT 522
QY 361 ccagagaagagctgt 420
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Db 523 CCAGAGAGAGT 582
QY 421 ttccgcacatcgt 480
|||||
Db 583 TTCCTCATGATGCTGT 642
QY 481 gacgagcagcagagctgt 540
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Db 643 GACGAGCAGCAGAGATTCAGTGCATCATCATCATCATCATCATCATCATCATCAT 702
QY 541 tgcgcac 600
Db 703 TGGCACAACCGGCTGT 762
QY 601 ggggacctgtggcg-tggaagtgcgagcgaagcgaagcagcagcagcagcagcagc 659
Db 763 ggggacctgtggcg-tggaagtgcgagcgaagcgaagcagcagcagcagcagcagc 821
QY 660 gctgcacgacatcc 671
Db 822 gctgcacgacatcc 833

RESULT 13
AL520223 908 bp mRNA EST 13-FEB-2001
LOCUS AL520223 LTI_NFL004_NBC2 Homo sapiens cDNA clone CSDB006Y103 5
DEFINITION prime, mRNA sequence.
ACCESSION AL520223
VERSION AL520223.1 GI:12783716
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 908)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 908
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1db="CSDB006Y103"
/clone_1db="LTI_NFL004_NBC2"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Ling Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610


```

OY 964 gccacattctgtcgagcaagaagcacaacatcctgagtgttgcacggcaattgaac 1023
Db 344 GCCAACTGTTGCTGAGCAAGAGGCCAAAACATCTGATGTTGCACGGCAGCTTAAC 285
OY 1024 gatgccattaa 1035
Db 284 GATGCCATTAA 273

RESULT 15
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DEFINITION AUI32868 NT2RP4 Homo sapiens cDNA clone NT2RP4000750 5', mRNA
sequence:
ACCESSION AUI32868
VERSION AUI32868.1 GI:109993407
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (Bases 1 to 812)
AUTHORS Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J.,
Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and
Isogai,T.
HRI human cDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y.,
Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano
,S., Masuho,Y., Isogai,T.)
Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
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/clone_lib="NT2RP4"
/cell_type="teratocarcinoma"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2 weeks retinoic acid (RA) induction."
BASE COUNT 193 a 226 c 241 g 152 t
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Best Local Similarity 99.2%; Pred. No. 1.9e-152;
Matches 634; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
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OY 61 gtcgtgcaacatgtgaaagcctcgtacccctggccctgcagcttgaatcatctcgtatgctc 120
Db 235 GTGCTGCAACATGTGAAGCGCTGTAACCTGGCGTGCAGATTGAATCATTTGATATGTC 294
OY 121 acccaaggagcaagaatcttctgtatctgcacctcctaagaatgagagaaaaagcctgttt 180
Db 295 ACCCAAGGAGCAAGATCTTGTGATCTGCACCTCTCAAGATTGGAGAGAAAAAGCCTGTTT 354
OY 181 accaaggagcttgacacatgcccctgagagaagaatgaagtgaacctgttgcactccttg 240
Db 355 ACCAAGGAGCTTGAACATGCGCTCGAGAGAAATGAAGTGCACCTGCTTCACTCCTTG 414

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OY 241 aaggacctgccacctgtgtcttcctccttggtcttcaccatcggagccatctgcaagcggaa 300
Db 415 AAGGACCTGCCCACTGTGCTTCTCCTGACTTCACCATCGGAGGCATCTGCAACGGGAA 474
OY 301 aacctcatatgctgtgtgtcttcacccaattgtttggaagaccctagaaccctg 360
Db 475 AACCTCATATGATGCTGTGTGCTTTCACCCCAAAATTTGTTGGAAACCTTGAAACCTTG 534
OY 361 ccagagaagaagtgtgtgtggaacacagctccctcgcgaagaagcagccatgcaagaaga 420
Db 535 CCAGAGAAGAAGTGTGTGTGGGAACCACTCCTCGGAAGAGCCACCTGCAGAGAAAG 594
OY 421 ttcccgatctggaagtcgaagatattcgagggaacccctcaacaccggcttcggaagctg 480
Db 595 TTCCCGATCTGGAGTTCAAGAGTATTCGGGAACCTCAACACCCGACTTCGGAAGCTG 654
OY 481 gacgagcagcagagttcagtgccatcaccctcgtggaacagctgagcctcagcagatgggc 540
Db 655 GACGAGCAGCAGAGTTCAAGTCCATCATCTGCGCAACAGCTGCCCTGCACGCCATGSGC 714
OY 541 tggcacaaccgggt-tggcagaatcctgaccctgaagaatgcatgatatgcttgggcca 599
Db 715 TGCCACAACCGGCTGGGGGCAATCTTCGACCCCTGAGGAATGATGATGCTGTGGCCA 774
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:37:53 ; Search time 90.47 Seconds
(without alignments)
2165.768 Million cell updates/sec

Title: US-09-601-138-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 segs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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Issued Patents NA: *
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5: /cgn2_6/pdata/1/ina/PCITUS.COMB.seq: *
6: /cgn2_6/pdata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41.6	4.0	729	1 US-08-599-480-3	Sequence 3, Appl 1
2	36.2	3.5	290	1 US-08-030-731A-41	Sequence 41, Appl 1
3	36.2	3.5	290	1 US-08-030-731A-42	Sequence 42, Appl 1
4	36.2	3.5	304	1 US-07-696-551B-12	Sequence 12, Appl 1
5	35.6	3.4	7218	1 US-08-232-463-14	Sequence 14, Appl 1
6	34.8	3.4	1889	2 US-08-946-241B-1	Sequence 1, Appl 1
7	34.8	3.4	1889	2 US-08-946-241B-8	Sequence 8, Appl 1
8	34.8	3.4	1889	3 US-09-309-053-1	Sequence 1, Appl 1
9	34.8	3.4	1889	3 US-09-309-053-8	Sequence 8, Appl 1
10	34.4	3.3	2502	1 US-08-073-384C-7	Sequence 7, Appl 1
11	34.4	3.3	2502	1 US-08-254-359A-7	Sequence 7, Appl 1
12	34.4	3.3	2502	1 US-08-483-043-7	Sequence 7, Appl 1
13	34.4	3.3	2502	1 US-08-481-238-7	Sequence 7, Appl 1
14	34.4	3.3	2502	2 US-08-471-066B-7	Sequence 7, Appl 1
15	34.4	3.3	2502	2 US-08-484-956-7	Sequence 7, Appl 1
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17	34.4	3.3	2502	2 US-08-599-491-7	Sequence 7, Appl 1
18	34.4	3.3	2502	2 US-08-756-386-7	Sequence 7, Appl 1
19	34.4	3.3	2502	2 US-08-823-516-7	Sequence 7, Appl 1
20	34.4	3.3	2502	3 US-08-682-853A-7	Sequence 7, Appl 1
21	34.4	3.3	2502	3 US-08-759-038-7	Sequence 7, Appl 1
22	34.4	3.3	2502	3 US-08-758-314-7	Sequence 7, Appl 1
23	34.2	3.3	510	1 US-07-918-953-7	Sequence 7, Appl 1
24	34.2	3.3	510	1 US-08-081-661-7	Sequence 7, Appl 1
25	34.2	3.3	729	4 US-09-140-804-10	Sequence 10, Appl 1
26	34.2	3.3	2793	1 US-08-209-747-1	Sequence 1, Appl 1
27	34.2	3.3	2793	1 US-08-458-298-1	Sequence 1, Appl 1

28	33.6	3.2	2121	4 US-09-358-683-1	Sequence 1, Appl 1
29	33.6	3.2	2276	1 US-08-202-389-11	Sequence 11, Appl 1
30	33.6	3.2	2394	4 US-08-797-358B-1	Sequence 1, Appl 1
31	33.6	3.2	2790	1 US-08-018-129-4	Sequence 4, Appl 1
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33	33.4	3.2	359	3 US-08-589-028-3	Sequence 3, Appl 1
34	33.4	3.2	359	3 US-08-784-582-3	Sequence 3, Appl 1
35	33.4	3.2	359	4 US-08-785-271-3	Sequence 3, Appl 1
36	33.4	3.2	11219	1 US-07-642-734C-1	Sequence 1, Appl 1
37	33.4	3.2	11219	3 US-08-435-009A-1	Sequence 1, Appl 1
38	33.4	3.2	44377	2 US-08-804-227C-7	Sequence 7, Appl 1
39	33.4	3.2	44377	2 US-08-804-198-1	Sequence 1, Appl 1
40	33.2	3.2	1201	6 5252556-2	Patent No. 5252556
41	33	3.2	281	1 US-07-764-659D-12	Sequence 12, Appl 1
42	33	3.2	281	1 US-07-764-655D-13	Sequence 13, Appl 1
43	33	3.2	281	6 5514646-1	Patent No. 5514646
44	33	3.2	3579	1 US-08-674-168-15	Sequence 15, Appl 1
45	33	3.2	3579	3 US-08-985-908-18	Sequence 18, Appl 1

ALIGNMENTS

RESULT 1
US-08-599-480-3/c
; Sequence 3, Application US/08599480
; Patent No. 5753459
; GENERAL INFORMATION:
; APPLICANT: Blanco, David R.
; APPLICANT: Miller, James N.
; APPLICANT: Lovett, Michael A.
; APPLICANT: Champion, Cheryl I.
; APPLICANT: Tempst, Paul J.
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF A
; TITLE OF INVENTION: T. Pallidum RARE OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,480
; FILING DATE: 23-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Learn, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: 07419/018001 (CIP of 016001)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: TROMP2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
; US-08-599-480-3

Query Match 4.0%; Score 41.6; DB 1; Length 729;
 Best Local Similarity 47.3%; Pred. No. 0.0058;
 Matches 125; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 56 acagtcggtggaacatctgaagcctcgtaccctgctcagcttggaatcctcta 115
 Db 428 AAACCTCGAGCGAGTACTGATATACCTGCACCCACACACAGTCGAACCCACTAC 369
 QY 116 tctcacacacagggagcaagatctctgaatcagcactctcctcaaatgaggagaaagcc 175
 Db 368 ACCCAGCAGGAGGGGATCTCGTATACCTGATACCACTTAACTAGTCCAGCCAG 309
 QY 176 tgttaccagaagagcttgaaatcgtccctgagagaagatgaagtgagactgtgtcact 235
 Db 308 TTATTCCTCTGTGATTTGAATTCGACTCTACTCCGATGAACGGGCTTCCTGTCTTC 249
 QY 236 ccttgaagagacctgctcctcctcctcctcctcctcctcctcctcctcctcctcctc 295
 Db 248 CCTTGCACGAGCCCGCATGGCAACCGCTGTGCGCATGCCCTCGAATACTTGAGGATA 189
 QY 296 gggagaaacccctcgtgtgtgtg 319
 Db 188 GCGAGCCCTTTGTGATGAATTTG 165

RESULT 2
 US-08-030-731A-41
 ; Sequence 41, Application US/08030731A
 ; Patent No. 5426036
 ; GENERAL INFORMATION:
 ; APPLICANT: Koller, Klaus-Peter
 ; APPLICANT: Rless, Guenther Johannes
 ; APPLICANT: Uhlmann, Eugen
 ; APPLICANT: Walmeier, Holger
 ; TITLE OF INVENTION: Processes for the Preparation of Foreign
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flinagan, Henderson, Farbow, Garrett &
 ; ADDRESS: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/030.731A
 ; FILING DATE: 12-MAR-1993
 ; CLASSIFICATION: 435
 ; PRIORITY INFORMATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/189,840
 ; FILING DATE: 03-MAY-1988
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/430,622
 ; FILING DATE: 01-NOV-1989
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/687,610
 ; FILING DATE: 19-APR-1991
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/735,757
 ; FILING DATE: 29-JUL-1991
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 37 14 866.4
 ; FILING DATE: 05-MAY-1987
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 38 37 273.8
 ; FILING DATE: 03-NOV-1988

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 39 27 449.7
 ; FILING DATE: 19-AUG-1989
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 40 12 818.0
 ; FILING DATE: 21-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kirschner Michael K.
 ; REGISTRATION NUMBER: 34,851
 ; REFERENCE/DOCKET NUMBER: 02481-0593-02000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-408-4000
 ; TELEFAX: 202-408-4400
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 290 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-030-731A-41

Query Match 3.5%; Score 36.2; DB 1; Length 290;
 Best Local Similarity 46.6%; Pred. No. 0.15;
 Matches 116; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 485 agcagagagatcagtgccatcaccctcgcacacagctgctcagcgcatggctgac 544
 Db 20 ACCAGCAGCTGTGGGCTCTCCACCTAGTGGAAGCTCTCTACGTGTGTGGGGAGAC 79
 QY 545 acaaccgggttgagagatccctgcacccctgagagatcagctatgctgtggtggcagg 604
 Db 80 GCTTCTTACACACCAAGCAAGCCCGGAGAGAGACCTCAGGTGGGAGGTGG 139
 QY 605 ccttggtgctggaagtgcagcaagagacagacatcttgatctgtgtgtgtgtgtg 664
 Db 140 AGCTGGGCGGGGCGCTGCGCAGCAACCTGCAAGCCCTTGCGGTGGAGGCTCCCTGC 199
 QY 665 acgatccagagatctgtctgcctgcatcgtctgaagagggccttcctgaagcaccctgag 724
 Db 200 AGAGCGCGCATCGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 259
 QY 725 gagggctgca 733
 Db 260 ACTACTGCA 268

RESULT 3
 US-08-030-731A-42/c
 ; Sequence 42, Application US/08030731A
 ; Patent No. 5426036
 ; GENERAL INFORMATION:
 ; APPLICANT: Koller, Klaus-Peter
 ; APPLICANT: Rless, Guenther Johannes
 ; APPLICANT: Uhlmann, Eugen
 ; APPLICANT: Walmeier, Holger
 ; TITLE OF INVENTION: Processes for the Preparation of Foreign
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flinagan, Henderson, Farbow, Garrett &
 ; ADDRESS: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25


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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,711A
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/189,840
FILING DATE: 03-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/430,622
FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,610
FILING DATE: 19-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,757
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 37 14 866.4
FILING DATE: 05-MAY-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 38 37 273.8
FILING DATE: 03-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 39 27 449.7
FILING DATE: 19-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 818.0
FILING DATE: 21-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kirschner Michael K
REGISTRATION NUMBER: 34,851
REFERENCE/DOCKET NUMBER: 02481-0593-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
FEATURE:
NAME/KEY: misc.feature
LOCATION: 5..290
OTHER INFORMATION: /note="Sequence ID No. 5426036 42 is
OTHER INFORMATION: Complementary to Sequence ID No. 5426036 41 at positions
OTHER INFORMATION: 5-230 of Sequence ID No. 5426036 41."
US-08-030-731A-42

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Query Match	3.5%	Score 36.2	DB 1	Length 299
Best Local Similarity	46.6%	Pred. No. 0.15		
Matches 116	Conservative	0	Mismatches 133	Indels 0
			Gaps	0
OY	485	agcagcagagatcattgcatcatcatctctgcaacagcctgagcctgcaagcagatggctcgc	544	
Db	275	ACCGACACCTGTGGCGCTCCACCTAGTGGAGGCTCTACCTGGTGGCGGAGGAG	216	
OY	545	acaaacgggttgtaggcagatctctgcaaccctgaaagaaatgcatatgatctgtgtgtgtgacgaagg	604	
Db	215	GCTTCTTCTACACACCCAGAGACCCGCCGGGAGGACGAGAGACCCCTCAGTGGGCGAGGTGG	156	
OY	605	cccttgagcgttgaaagtgcgaagcaagagacatcttgatctcgtgtgtgtgtgc	664	
Db	155	AGCTGGGGGGGGGCGCTGGCGGAGCGAGCTCTACACCCCTGGCGCTGGAGCGCTCCCTGC	96	
OY	665	agcatcccggaagctctgcttcgtcatcgtcgtgaaaggccctctcgtggaaccttgaaag	724	
Db	95	AGAGCGCGGCGATCTGTGAGACACTGCTGACACGACATCTGCTCCTCTACACAGTGGAGA	36	
OY	725	gaagcctgcga	733	

```

Db          35 ACTACTGCA 27          |||||
                                           |||||
RESULT      4
US-07-696-551B-12
: Sequence 12, Application US/07696551B
: Patent No. 5232841
GENERAL INFORMATION:
APPLICANT: Hashimoto, Tamotsu
APPLICANT: Tsujimura, Atsushi
APPLICANT: Ueda, Shigezo
TITLE OF INVENTION: Process for Preparing Peptide
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
:
: STREET: 1300 I Street, N.W., Suite 700
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/PC-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/696,551B
FILING DATE: 19910509
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-122166
FILING DATE: 11-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-334575
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence M. Lavin, JT.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 2481-1070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-696-551B-12

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Query March	3.5%	Score 36.2;	DB 1;	Length 304;
Best Local Similarity	46.6%;	Pred. No. 0.12;		
Matches 116;	Conservative 0;	Mismatches 133;	Indels 0;	Gaps 0;
QY	agagcagagaggttcagatcgacatcatccatgcgaacagcgcgcgcctcgaagcatgtgctgc	544		
DB	43 ACCACACACCTCTGCGCTCCACACTAGTGGAAAGCTCTACTCTGCTGGGGAGACGAG	102		
QY	545 acaacgcggtgtggagcatccatgcgaacccctggagaaatgcatgtatgctgtgacgaaggg	604		
DB	103 GCTTCTTCTACACACCCACAGACCCCGCGGAGACAGAGAACCTCTACAGTGGCGACATCG	162		
QY	605 ccttggtgcgtgtggaagtgtgcagagccaaggaacacagaaatcttgatctctgtgtgtgtgc	664		
DB	163 AGCTGGGGGGGGCCCTGGGGGCGCAGGACGCTTCAACCCCTTGCCCTGTAGAGAGGCTCCCTG	222		
QY	665 agcatcccgagactctgtctgtcatctcatctgtgaaaggcccttcctgtgaaggaccttggaa	724		
DB	223 AGAAGCCCGCATCTGTGGACATCTGTGCACCGCATCTGTCTCTTACCACTACGTGAGA	282		

Oy 725 gaggtgca 733
Db 283 ACTACTGCA 291

RESULT 5

US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHERLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)856-9300
TELEFAX: (703)863-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: PT29PT-F18
US-08-232-463-14

Query Match 3.4%; Score 35.6; DB 1; Length 7218;
Best Local Similarity 3.3%; Pred. No. 1.1;
Matches 11; Conservative 184; Mismatches 143; Indels 0; Gaps 0;

Oy 340 gggagaccctgagaaacctccagagagagtggtggaaccgctccctcgaga 399
Db 1386 RRR 1327
Oy 400 gcagccacgtcagagaagltccgcacgtcagagtcagagtcgtgggaacctc 459
Db 1326 RRR 1267
Oy 460 aacacccgctcgagagctcgagcagcagcagagtcagtcacatccctgcaaca 519
Db 1266 RRR 1207
Oy 520 gctggcctcgacgacatggtgacacaccgggtggtgcagatcctcgacccctgagaa 579

Db 1206 RRR 1147
Oy 580 tgcgtatgctgtggccagggggtcgtgagtgagtcagcaggaaccagac 639
Db 1146 RRR 1087
Oy 640 atcttgatctgtgggtgtgctgcacgacatcccgagac 677
Db 1086 RRR 1049

RESULT 6

US-08-946-241B-1/C
Sequence 1, Application US/08946241B
Patent No. 5928941
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: MCA/Nulty, Megan M.
TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,241B
FILING DATE: 07-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,035
FILING DATE: 05-NOV-1996
APPLICATION NUMBER: 60/027,521
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 05433/027001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1889 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 434...1843
US-08-946-241B-1

Query Match 3.4%; Score 34.8; DB 2; Length 1889;
Best Local Similarity 52.8%; Pred. No. 0.99;
Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Oy 608 tgggtgtgaggtcgagcaggaagacatctgatactgtgtgtgtgtgtgtgtgtgt 667
Db 1434 TGGGATGGAAGCGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1375
Oy 668 atccgagacgtctgtctgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 727
Db 1374 TCCTAAGACCAAGGTGCGGAGTGTCTGCTGGAGCTGCCGCCAGGCGAAGTGC 1315

QY 728 gctgcagctgctcagtagccgt 749
||||| ||||| |||||
DB 1314 TGTGACGCGGCGGTGCGCAT 1293

RESULT 7

US-08-946-241B-8/C
; Sequence 8, Application US/08946241B
; Patent No. 5928941
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: MCA'Nulty, Megan M.
; TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/946,241B
; FILING DATE: 07-OCT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,035
; FILING DATE: 05-NOV-1996
; APPLICATION NUMBER: 60/027,521
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Creason, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 05433/027001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1889 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 407...1843
US-08-946-241B-8

Query Match 3.4%; Score 34.8; DB 2; Length 1889;
Best Local Similarity 52.8%; Pred. No. 0.99;
Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 608 tgggcgtggaagctgcagcgaagacacatcttgatctgtgtgtgtgtgcacg 667
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1434 TGGGGATGGAAGCGCGGAGAGAGCGGAGGAGGTGACAGTCCCTCTCTCAGCACT 1375
QY 668 atcccgagactctgctgcgtgcacgtcgtgaagagccttcctgaagcacttgaaagag 727
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1374 TCTTCAGACCCAGGCTCGGGGTAGTCTGCTGGGAGCTGCGCCGCCAGGGGAAAGTCG 1315
QY 728 gctgcagctgctcagtagccgt 749
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1314 TGTGACGCGGCGGTGCGCAT 1293

RESULT 8
US-09-309-053-1/c

; Sequence 1, Application US/09309053
; Patent No. 6077933
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: MCA'Nulty, Megan M.
; TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,053
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/946,241
; FILING DATE: 07-OCT-1997
; APPLICATION NUMBER: 60/030,035
; FILING DATE: 05-NOV-1996
; APPLICATION NUMBER: 60/027,521
; FILING DATE: 07-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Creason, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 05433/027001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1889 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 434...1843
US-09-309-053-1

Query Match 3.4%; Score 34.8; DB 3; Length 1889;
Best Local Similarity 52.8%; Pred. No. 0.99;
Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 608 tgggcgtggaagctgcagcgaagacacatcttgatctgtgtgtgtgtgcacg 667
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1434 TGGGGATGGAAGCGCGGAGAGAGCGGAGGAGGTGACAGTCCCTCTCTCAGCACT 1375
QY 668 atcccgagactctgctgcgtgcacgtcgtgaagagccttcctgaagcacttgaaagag 727
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1374 TCTTCAGACCCAGGCTCGGGGTAGTCTGCTGGGAGCTGCGCCGCCAGGGGAAAGTCG 1315
QY 728 gctgcagctgctcagtagccgt 749
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1314 TGTGACGCGGCGGTGCGCAT 1293

RESULT 9
US-09-309-053-8/c
; Sequence 8, Application US/09309053
; Patent No. 6077933
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: MCA'Nulty, Megan M.

1 ADDRESS: HAVERSTOCK, MEDLEN & CARROLL,
2 STREET: 220 Montgomery Street, Suite 2200
3 CITY: San Francisco
4 STATE: California
5 COUNTRY: United States of America
6 ZIP: 94104
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: Patent In Release #1.0, Version #1.25
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/073,384C
15 FILING DATE: 04-JUN-1993
16 CLASSIFICATION: 536
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 07/986,330
19 FILING DATE: 07-DEC-1992
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Carroll, Peter G.
22 REGISTRATION NUMBER: 32,837
23 REFERENCE/DOCKET NUMBER: FORS-00613
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: 415/705-8410
26 TELEFAX: 415/397-8338
27
28 INFORMATION FOR SEQ ID NO: 7:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 2502 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34
35 US-08-073-384C-7

Query Match	Best Local Similarity	3.38%	Score 34.4	DB 1	Length 2502
Matches 128	Conservative	44.0%	Pred. No. 1.5	Mismatches 163	Indels 0
				Gaps 0	
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QY 473	ggaagctctgacagacagacagagatcagttgcatacatctcggacaacagcgtgcctcagc				532
Db 1292	ACCAGAGAGGTGGAGAAAGCCCTTTCGCGGTCCTGTGCCACATGGAAGGCCACGGGGGTC				1351
QY 533	gcatggcgtcgagcaaacacggggtctggcgcgatcctgcaccccttgaaatgcatgatgtctg				592
Db 1352	GCGTGGACGTGGCTTACCTCCACGGGCCCTTCCCTGGAGTGGCGGAGAGATCCGCCGCC				1411
QY 593	tgggccaaggggacctctggcgctggaagtgcgaagcgaagacagacatcttgatctgg				652
Db 1412	TCGAGAGAGAGAGTCTTCGCCCTGGCGGCGCACCCCTTCAACCTCAACTCCGGGACACAC				1471
QY 653	tgggtgtgtgcagatcaccgaagatcgtcttgctgtcaccgtctgaaagg				703
Db 1472	TGCAAGGCTGCTCTTTACACAGCTNGGAGCTTCCCGCCATCGGCAAGACGG				1522

RESULT 11
 US-08-254-359A-7
 : Sequence 7, Application US/0824359A
 : Patent No. 5614402
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: DAHLBERG, JAMES E.
 : APPLICANT: LYAMICHEV, VICTOR I.
 : APPLICANT: BROW, MARY ANN D.
 : TITLE OF INVENTION: 5' NUCLEASES DERIVED FROM THERMOSTABLE
 : TITLE OF INVENTION: DNA POLYMERASE
 : NUMBER OF SEQUENCES: 40
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
 : STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,359A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-254-359A-7

Query Match 3.3%; Score 34.4; DB 1; Length 2502;
Best Local Similarity 44.0%; Pred. No. 1.5;
Matches 128; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 413 agagaaggttcgcgcacatcgtgagttcagaagatcctcggygaacctcaaccggcttc 472
DB 1232 AGAGGCTCTTCGACCAACCTNNNGACGCGCTTGAGGGGAGAGAGGCTCTTGGGCTTT 1291
QY 473 ggaagctgagagcaagagagttcagtcacatcctcggcaacagctgagctgcagc 532
DB 1292 ACCAGGAGGTGAGAGAGCCCTTCCGGGCTCCTGACATGAGGCCACGGGGGTMC 1351
QY 533 gcatgggctgacacaaacgggtgtggagatcctgacccctgaggaatgcatgtatctg 592
DB 1352 GCGTGGAGCTGGCTTACCTCCAGGCCCTTTCCTGAGGTGCGGAGAGATCCGCCGCC 1411
QY 593 tgggccaaggggaccttggcgctggaagtgcagacaaagaccagagacatcttgatctgg 652
DB 1412 TCGAGAGAGAGGTCTTCGCGCTGCGGCCACCCCTTCAACCTCAATCCGGGAGCAGC 1471
QY 653 tgggtgtgctgcagatcccgagacctgtctgcctgcatctgctgaagg 703
DB 1472 TGGAAAGGCTCTTTGACGAGCTMGGGGCTTCCGCCATCGGCAAGACGG 1522

RESULT 12
US-08-483-043-7
Sequence 7, Application US/08483043
Patent No. 5691142
GENERAL INFORMATION:
APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,043
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-00613
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
TELEFAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-043-7

Query Match 3.3%; Score 34.4; DB 1; Length 2502;
Best Local Similarity 44.0%; Pred. No. 1.5;
Matches 128; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 413 agagaaggttcgcgcacatcgtgagttcagaagatcctcggygaacctcaaccggcttc 472
DB 1232 AGAGGCTCTTCGACCAACCTNNNGACGCGCTTGAGGGGAGAGAGGCTCTTGGGCTTT 1291
QY 473 ggaagctgagagcaagagagttcagtcacatcctcggcaacagctgagctgcagc 532
DB 1292 ACCAGGAGGTGAGAGAGCCCTTCCGGGCTCCTGACATGAGGCCACGGGGGTMC 1351
QY 533 gcatgggctgacacaaacgggtgtggagatcctgacccctgaggaatgcatgtatctg 592
DB 1352 GCGTGGAGCTGGCTTACCTCCAGGCCCTTTCCTGAGGTGCGGAGAGATCCGCCGCC 1411
QY 593 tgggccaaggggaccttggcgctggaagtgcagacaaagaccagagacatcttgatctgg 652
DB 1412 TCGAGAGAGAGGTCTTCGCGCTGCGGCCACCCCTTCAACCTCAATCCGGGAGCAGC 1471
QY 653 tgggtgtgctgcagatcccgagacctgtctgcctgcatctgctgaagg 703
DB 1472 TGGAAAGGCTCTTTGACGAGCTMGGGGCTTCCGCCATCGGCAAGACGG 1522

RESULT 13
US-08-481-238-7
Sequence 7, Application US/08481238
Patent No. 5795763
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:

```

ADDRESS: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,238
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-481-238-7

Query Match
Best Local Similarity 3.3%; Score 34.4; DB 1; Length 2502;
Matches 128; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

413 agagaaagtcgcgcagatcggaggtcagagatcggggaagaccacacccggcttc 472
1232 AGAGGCTCTTCNGAACCTNNNGCAGCCCTTGAGGGGAGAGAGCTCTTGGCTTT 1291
473 ggaagctcgaagcagcagcagagatcagtcacatcctcgcaacagctcgctcgagc 532
1292 ACCAGAGGCTGAGAGAGCCCTTTCCTCCGGCTCCGCCCATGAGGCCAGGGGGTNC 1351
533 gcatcgagcgcagcagcagcgggttcggcagatcctgcacccctcgaggaatcagtgatcg 592
1352 GGCTGAGCTGACCTACCTCCAGGCCCTTTCCTGAGGTGGGAGAGATCCGCCGCC 1411
593 tgggcagggggccttcggcgctggaagtgcgagccaaagcagcagcattcgatctgg 652
1412 TCGAGAGGAGGCTCTTCCTCCGCGCCGCCACCCCTTCAACCTCAACCTCCCGGACGACG 1471
653 tgggtgctgcagcagatcccgagatcctgcttcgctgcagtcgctgaagg 703
1472 TCGAAGGCTGCTCTTTCAGCAGCTNGGCTTCCCGCCATCGGCAGACGCG 1522

RESULT 14
US-08-471-066B-7
Sequence 7, Application US/08471066B
Patent No. 5837450
GENERAL INFORMATION:
APPLICANT: Dahlberg, James E.
APPLICANT: Lyanichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: 5' Nucleases Derived From Thermostable
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
```

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COUNTRY: United States of America
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,066B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-01800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-471-066B-7

Query Match
Best Local Similarity 3.3%; Score 34.4; DB 2; Length 2502;
Matches 128; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

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1292 ACCAGAGGCTGAGAGAGCCCTTTCCTCCGGCTCCGCCCATGAGGCCAGGGGGTNC 1351
533 gcatcgagcgcagcagcagcgggttcggcagatcctgcacccctcgaggaatcagtgatcg 592
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593 tgggcagggggccttcggcgctggaagtgcgagccaaagcagcagcattcgatctgg 652
1412 TCGAGAGGAGGCTCTTCCTCCGCGCCGCCACCCCTTCAACCTCAACCTCCCGGACGACG 1471
653 tgggtgctgcagcagatcccgagatcctgcttcgctgcagtcgctgaagg 703
1472 TCGAAGGCTGCTCTTTCAGCAGCTNGGCTTCCCGCCATCGGCAGACGCG 1522

RESULT 15
US-08-484-956-7
Sequence 7, Application US/08484956
Patent No. 5843654
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYANICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.
APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF P53 MUTATIONS
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Maximum Match 100%

Listing first 45 summaries

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 Db 881 GCCTCTGT 939
 QY 841 aagatgt 900
 Db 940 AAGATGT 998
 QY 901 caagagacatgt 936
 Db 999 CAAGAGA-CATGAGGCTA-CATCATGTCTCCGCC 1032

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 prime, mRNA sequence.
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 VERSION AL524270.1 GI:12787763
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 882)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with NotI and
 cloned into the NotI and EcoRV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact: Feng Liang Life
 Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email: fliang@life.techn.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 205 a 236 c 262 g 178 t 1 others
 ORIGIN

Query Match 75.28; Score 837.4; DB 105; Length 882;
 Best Local Similarity 99.28; Pred. No. 4.5e-214;
 Matches 852; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
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QY 313 tcttgaagaagcttgcacactgtgtcttccctgtgtcttcaacatcagagacatcgaag 372
 Db 61 TCCTTGAAGAGCTGCGCCACTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
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 Db 121 CGGGAAGAACCCCTATATATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
 QY 433 accctgt 492
 Db 181 ACCCTGT 240
 QY 493 agaaatttcccgatctgt 552
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 QY 553 aagctgt 612
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 QY 613 atggctgt 672
 Db 361 ATGGCTGT 420
 QY 673 ggcacagggggt 732
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 QY 733 ggt 792
 Db 481 GGT 540
 QY 793 caactgt 852
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 QY 853 ctgtactgt 912
 Db 600 CTGTACTGT 659
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 Db 840 CAGCTTAACGATGCCATT 858

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 LOCUS AL557370 942 bp mRNA EST 16-FEB-2001
 DEFINITION AL557370 LTI_FL012_TCI Homo sapiens cDNA clone CS0DH004YPI3 5 prime
 , mRNA sequence.
 ACCESSION AL557370
 VERSION AL557370.1 GI:12900909
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 942)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)


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Oy 353 ccatcggagccatctcgaaagcgggaaacccctcatgatgctgtgtcttcaacccaat 412
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Db 122 CCATCGAGGCACTCTCGAAGCGGAAACCCATGATGCTGTCTTCCACCAAAAT 181
Oy 413 ttgttggaaagacccttagaaacccctccagagaagaagtggttggaacccagctccctgc 472
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Db 182 TTGTTGGAGAACCCCTAGAAACCCCTCCAGAGAAAGTGTTGGTGGAAACCAAGCTCCCTGCG 241
Oy 473 gaagaagaagcccgctgcagagaagaagttcccgcatctggaatcaagaagatctcgggaa 532
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Db 242 GAAGAGAGAGCCCGAGCTGCAAGAAAGTTCCTCCATCTGAGTTACAGAGATTCGGGGAA 301
Oy 533 accctaaaccccggtcttggaagcttgaaagcagcagaagatctcagtcacatccctgc 592
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Db 302 ACCTCACACACCCCGCTTCCGGAAGCTGACAGACACAGAGAGTTCAGTCCATCATCTCG 361
Oy 593 caaagctggcctgcagcagcagctgagcacaacccgggttgccagaatctctcacccctg 652
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Oy 893 atggcatcagaagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 952
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Oy 953 ctgagatgacccacagtggtgtagcagcagcagcagcagcagcagcagcagcagcagcagc 1008
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RESULT 5
LOCUS BG469642 835 bp mRNA EST 21-MAR-2001
DEFINITION 602533692P1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661422 5',
            mRNA sequence.
ACCESSION BG469642
VERSION BG469642.1 GI:13401917
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 835)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
            Email: cgrpb-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            DNA Sequencing by: NIH Intramural Sequencing Center
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL etc.
            http://image.llnl.gov
            Plate: LCM1460 row: g column: 23
            High quality sequence stop: 824.
            Location/Qualifiers

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/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 194 a 229 c 250 g 162 t
ORIGIN

Query Match 65.1%; Score 724.4; DB 154; Length 835;
Best Local Similarity 99.6%; Pred. No. 9.8e-184;
Matches 747; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Db 85 CACAGACCTACTTCTCCAAAGCGGACCATGTCTGTAAACGGCATGCGCTGCACGCGG 144
Oy 61 gaagaaagaccccaagaatgagtgatgctgctggtggaacccgaagagcagctgtct 120
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Db 145 GAAGAAACAGGCCAAAGATGAGATGATTCGGTGGGTACCCCAAGACCAAGCTTGGT 204
Oy 121 cgtatcagaagcagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
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Db 205 CGCATACAGACGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 264
Oy 181 gaatcatctgcatgtccacacacagaggaagaatctctgtaactgcaatcttaagat 240
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Db 265 GAATCATGTGTAATGTCACACACAGGGGCAAAATTTGTATACTGCACCTCTTAAGATT 324
Oy 241 ggaagaaagagcctgttaccagaagagcttgaaatcctcctggaagaagaatgagtgac 300
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Db 325 GGAGAAAGAGGCTCTTTTACCAGAGGCTTGAAATCCTCTGAGAAAGATGAAAGGAC 384
Oy 301 ctgtgtgtcactctctgaagagcctgccaactgtgtctcctcctgctcagcagcagcagc 360
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Db 385 CTGTTGTTCACCTCTGAAGACCTGCCACTGTGCTCTCTCTGCTTCCATCGA 444
Oy 361 gccatctgaaagcgggaaacccatgatatgctgttcttcaacccaatctgttgg 420
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Db 445 GCATCTGCACGCGGAAACCTCATGATGCTGTGTCTTTCACCAAAATTTGTGGG 504
Oy 421 aagaccctagaacccctgcagagaagaatgttggatggaacacagctccctcgaagaaga 480
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Db 505 AAGACCTAGAAACCTCCAGAGAAAGTGTGTGGAAACACAGCTCCTCGGAAGAGCA 564
Oy 481 gccagctcagaagaatctccgcatctgagttcagagtgatcttgggggaaacccacac 540
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Oy 541 acccggtctggaagctggaagcagcagcagcagcagcagcagcagcagcagcagcagc 600
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Db 625 ACCCGGCTTGGAACTGAGACACACAGAGTTCAGTCCATCTCTGCAACACT 684
Oy 601 gccctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 660
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Db 685 GCGCTGACGCGATGCGCTGGCACACCGGGTTGGAGATCTGCAACCTTACGAAATGC 744
Oy 661 agtatgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 719
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Db 745 ATGTATGCTGTGTGGCCAGGGGCTTGGGGTGGAAATGTCGAGCAAGACAGAGACAT 804
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ACCESSION	AL561865		
VERSION	AL561865.1	GI:12909719	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 (bases 1 to 949)		
TITLE	Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization unpublished (2001)		
COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage bp 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.		
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	/tissue_type="neuroblastoma cells"		
	/lab_host="DH10B"		
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (41) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"		
BASE COUNT	196 a	277 c	265 g
ORIGIN		207 t	4 others
Query Match	63.9%	Score 711.4;	DB 106; Length 949;
Best Local Similarity	98.6%	Pred. No. 3.1e-180;	
Matches 756; Conservative	3; Mismatches	4; Indels	4; Gaps 4;
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407	caaaatttgttgggaagaccctagaaacccctccagagaagatgtgtgtggaacagct	466	
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OY	707	aggaccaggaacatcttgagcttgggtggtgtgtcgcagatccagaactctgttcgact	766
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OY	827	Tgcatacagatcatgaagagatcgggcaactctacctaacctgaagaaatctcgaagctcgaagc	886
Db	464	TGCATACAGCATGAAGAAGATGGCGAACCTGACTGACTGTGAGAGACTGTGAGATCTAGACG	405
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Db	344	ATGGCCCTGAGATGACCCACAGTTGCTGAGGATCATCTCTGTAACTTCACAGAGGCG	285
OY	1007	ccccgtttggtgtccccaagaacttttgagatcagctctggccaacttgtttgttgagcaagaag	1066
Db	284	CCCCGTTGGCTGCCACAGACTTGGCATCGCTGGCCACTGTGTGTGAGCCAAGAG	225
OY	1067	ccaaaacatctcgtgaatcgtgtcagcggccaattggaacgatgtccattaa	1113
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DEFINITION	BE561357	1136 bp MRNA	EST 15-AUG-2000
ACCESSION	601344923FI NIH_MGC_8 Homo sapiens CDNA clone IMAGE:3677764 5'		
VERSION	BE561357	mRNA sequence.	
KEYWORDS	BE561357.1 GI:9805077		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
COMMENT	NIH-MGC hlup://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabs-femail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov plate: LNCM53 row: n column: 05 High quality sequence stop: 714. location/Qualifiers		
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	/lab_host="DHIOB (Phage-resistan)"		
	/note="Organ: lymph; Vector: pOTBT; site_1: XhoI; site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."*		
BASE COUNT	280 a 298 c 341 g 217 t		

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Qy	774	tgaaggagccttcctgaaggcacccttgaaaggagccttcgaagtgtccagtagtcgtgac	833
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Qy	834	agcataagagatgagcgaactgtaccgtactgcgaagagctctgtagtctagaagcgtcaca	893
Db	808	AGCTATCAAGAGATGGCGCAACTGTACCTGACTGAGAGAGTGGAGTCTATAGACGGCTCAGA	867
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RESULT	9		
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DEFINITION	AU132868 NT2RP4 Homo sapiens CDNA clone NT2RP4000750 5', mRNA	EST	24-OCT-2000
ACCESSION	AU132868		
VERSION	AU132868		
KEYWORDS	AU132868.1 GI:10993407		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 812) Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y. and Isogai,T. HRI human CDNA project (Ota,T., Sugiyama,T., Ishii,S., Suzuki,Y., Saito,K., Yamamoto,J., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano ,S., Masuho,Y., Isogai,T.) Unpublished (2000) Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@hri.co.jp HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; CDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute		
JOURNAL			
COMMENT			
TITLE			
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Best Local Similarity	99.3%; Pred. No. 5,1e-114;		
Matches	712; Conservative 0; Mismatches 3; Indels 2; Gaps 2.		
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Db	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608
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/clone_lib="LTI_F1012.TCI"
/libuse_type="T cells from T cell leukemia"
/Note="Vector: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-stranded cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the PCMVSPORT 6 vector.
Library was constructed by life technologies. Contact :
Feng Liang Life Technologies, a division of Invitrogen
9800 Medical Center Drive Rockville, Maryland 20850, USA
Fax : (1) 301 610 8371 Email : fliang@life.com URL :
http://fulllength.invitrogen.com"
BASE COUNT      160 a      243 c      225 g      189 t      21 others
ORIGIN

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Query Match      61.3%; Score 682; DB 106; Length 838;
Best Local Similarity 95.4%; Pred. No. 2,4e-172;
Matches 702; Conservative 18; Mismatches 14; Indels 2; Gaps 2;

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QY 378 aaaccctcgtatgctgcttccacaaattctgtggaagaccctagaacct 437
|||||
DB 838 AACCCCTCATGATGCTKTTGTCTTTCACCCAAATTTGTT-GGAAGACCTAGAAACCT 780
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QY 438 gccagaagaagtctgctggaaccagctcctctggaagcagccagctgcagagaa 497
|||||
DB 779 GCCAGACAAGAGTGTGTGGAAACGCTCCTCGAAGACAGCCCACTGCCAGAA 720
|||||
QY 498 gtccgcactctggaattcaagagatctcgggaaacctcaaccggcttcggaagt 557
|||||
DB 719 GTTCCCATCTGAGCTTCAGAGTATTCGGGAAACCTCAACACCCGGCTTCGGAAGCT 660
|||||
QY 558 ggaacgaagcagaagctcagtcacatccctgcgaacagctgagctgcagcagat 617
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DB 659 GGAAGACACAGAGATTCAGTCCATCTCTGCAACACCTGCTGCAAGCCATGCG 600
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QY 618 ctggacacacacgggttggcgaatccctgcacacccctggaagatgcatgtatctg 677
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DB 599 CTGGACACACGGGTGGGAGATCTCTGCAACCTCAAGAAATGATGATCTGTGGCCA 540
|||||
QY 678 gggggccctggcgtggaagctgcagacgaagacacacacacacacacacacac 737
|||||
DB 539 GGGGGCTTGGCGGTGGAAGTGCAGGCCAGACAGACACATCTTGATCTGGTGGGT 480
|||||
QY 738 gctgcacgataccgagactctgtctgcctgcagctgaaaggcctctctgagga 797
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DB 479 GCTGCAGAGATCCCGAGACTCT-CTTGGCTGATGCTGTAAAGGCCCTTCTGAGCA 421
|||||
QY 798 ggaagaggcgtcgaagtgtgccagctgacatagcattagaagatgggcaactg 857
|||||
DB 420 GGAAGAGGCTGAGTGTCCAGTAGCCGTGCATACAGCATGAAAGATGGCCAACTGA 361
|||||
QY 858 cctgactggaagagctcgtgagctcagatagcattacaagaagacacatgagc 917
|||||
DB 360 CCTCACTGAGAGTCTGTGAGTCTAGACSGCCAGATMGCTACAAAGAGMCATGAGC 301
|||||
QY 918 taccatccatctgcccctggccagacatgaagatgcccctggaagatgaaccagtt 977
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DB 300 TACCATCCATGTCCTCCACCATGAAAGATGCGCTGTAGATACCCACAGTTGTGTA 241
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QY 978 calcatgctctaaacatccacagagcccaagtgtgctgcacgaagacttgagc 1037
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DB 240 CATCACTGCTGCTGATTCACGAGGGCCCACTTGGCTGCCAATACTTGGGCACT 181
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QY 1038 cctggcacaactctgtctgagcagaagagccaaataacccttgatgtctgacgg 1097
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DB 180 CCTGGCCCAAAATATGCTGAAGAAAGAAAGAAAGAAACATCTGATGTGACGAGCA 121
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QY 1098 gaacgagtcacataa 1113
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DB 120 TAACGATCCSATTRA 105

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RESULT 11
LOCUS BE547860
DEFINITION 601074758F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460575,
mRNA sequence.
ACCESSION BE547860
VERSION BE547860.1 GI:9776505
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (Bases 1 to 804)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the T.M.A.G.E. Consortium/LML at:
http://image.llnl.gov
Plate: ULAH8455 row: d column: 16
High quality sequence stop: 670.
FEATURES
source
location/Qualifiers
1..804
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="3460575"
/clone_lib="NIH_MGC_12"
/libuse_type="cervical carcinoma cell line"
/lab_host="DH10B"
/Note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

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BASE COUNT      171 a      226 c      235 g      172 t
ORIGIN
Query Match      60.3%; Score 671.4; DB 137; Length 804;
Best Local Similarity 94.0%; Pred. No. 1.7e-169;
Matches 742; Conservative 0; Mismatches 41; Indels 6; Gaps 4;
QY 86 tgattcgctggtaaccgcaagaccagctgtctgcacatacagaagcagtggtg 145
|||||
DB 1 TGATTGCGGTGGTACCCGCAAGACCGAGCTTGCTGCATACAGAGAGACAGTGTG 60
|||||
QY 146 caacatgaagcctgtgaacctgagcctgcagcttgaaatcatctatgctccacag 205
|||||
DB 61 CAACATTTGAAGCTCTGTAACCTGCTGCACTTGAATCATTTCTATGTCCACACAG 120
|||||
QY 206 gggaacaagattctgatactgcaactcttaagatttggagaaagacccgtttaca 265
|||||
DB 121 GGCACAAGATTTCTGATACCTGACTCTTAAGATTGAGAGAAACCTGTTTACCAAG 180
|||||
QY 266 agcttgacaatcccttgaaagaagaagatgagcctggtgtgtcaactccttgaag 325
|||||
DB 181 AGCTTAAATATCCCTTGAGAGAAATGAGACCTGGTGTTCACCTCTTGAAGGAC 240
|||||
QY 326 tggccactgtcttccctcctgctcaccatcgaaagcactctcaagcggaacccctc 385
|||||
DB 241 TGCCCACTGTGCTCTCTCTGCTTCAACATCGAGAGCAATCTCAAGCGGAAACCT 300
|||||
QY 386 atgatactgtgtcttcaaccataatttctgggaagacccctagaacccctgcaga 445
|||||
DB 301 ATGATGCTGTGTCTTTCACCAAAATTCGTTGGAGACACCTTGAAGAACCTTGC 360
|||||
QY 446 agagtggtggaaaccagctccctcgaaagacagccacagctgcagagaagaatccgc 505
|||||

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Db 361 AGAGTGGTGGGACACACTCCCTCCGAGAGACGCCACTGACAGAAAGTTCCCC 420
Oy 506 atctgaggtcaggagatctcggggaacccaacccggcttcggagctggagc 565
Db 421 ATCTGAGGTTTCAGAGATATTTCCGGGGAAACCTCAACCCCGGCTTCGAAAGCTGACGAC 480
Oy 566 aagagaggttcagtcacatcctctggcaagagctggccttcagcgatggagctggaca 625
Db 481 AGCAGAGGTTTCAGAGATATTTCCGGGGAAACCTCAACCCCGGCTTCGAAAGCTGACGAC 540
Oy 626 accggtctggcagatccctgcacacctgaagaaatgatatgtctgtggccaggggct 685
Db 541 ACCGGGTGGGGGAGATCTGACACCCGAGAGATGATATGCTGGGCGAGGGGCTT 600
Oy 686 tggcgtctggagctggagcgaaggaacagacatcttgatctgtgtgtgtgtgacg 745
Db 601 TCGGCGTGGAAAGTCCGACGACGCGCCAGACATCTTGATCTGTGTGTGTGTGTGACG 660
Oy 746 atccgagactctg--cttgcgtgacgtgta--aaggccttcctgaagcactggaa 801
Db 661 ATCCCGAGACTGTGCTTGGCTTGCATCTTACTAGAGGGGCTTCTGAGGACACTGAA 720
Oy 802 -ggaagctgagctgt-gccagtagccgtgcatagcagctgaagatggaggaactgac 859
Db 721 CCGATGCTGCGCTTGGCGCCGATACCTCTTCCGCTTCGCGCTGCTGCTGCTGCT 780
Oy 860 tgaactggag 868
Db 781 TGCTGCGACG 789

RESULT 12
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LOCUS AL520284 LRL_NFL004_NBC2 Homo sapiens cDNA clone CS0DB006YG07 3
DEFINITION Prime, mRNA sequence.
ACCESSION AL520284
VERSION AL520284.1 GI:12783777
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 919)
AUTHORS Li, W.-B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
1. 919
FEATURES
Source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="LRL_NFL004_NBC2"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 191 a 276 c 248 g 202 t 2 others
ORIGIN

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Query Match 59.2%; Score 659.2; DB 105; Length 919;
Best Local Similarity 98.7%; Pred. No. 3,26-166;
Matches 705; Conservative 1; Mismatches 4; Indels 4; Gaps 4;

Oy 400 ttaccccaaatcttgtaggaagaccctagaacccctgcagaggaagatgtgtggag 459
Db 918 YTTACCCCAAAATTTGTT-GGAAGACCTTAGAAACCTTGCCAGAAAGATGTGTGT-GGA 861
Oy 460 accagctccctggagagcagccagctgcagagaaagctccgcatctgaaatcag 519
Db 860 ACCAGCTCCCTGGAGAGACAGCCAGCTGCAGAGAAAGTTCCCGCATCTGGAGTTCCAG 801
Oy 520 agatctggggaacccccaacacccggcttcggaagctggagcagagcagagatcagt 579
Db 800 AGTATTC-GGGAAACCTCAACACCCGCTTCGGAAGCTGGACAGACAGAGAGTTAGT 742
Oy 580 gcaatcctctgcaaacagctgtgctgcagcgatggctgtgcacacacgggtgtggcag 639
Db 741 GCATCATCTGTGCAACAGCTGCGCTGCAGCGCATGGGCTGCACAAACCGGTGGGCGAG 682
Oy 640 atctgcacccctgaggaatgatatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 699
Db 661 ATCTGCACCCCTAGAGATGATGATGCTGTGGGCGACAGGGGCTTGGGCTGGAAGT 622
Oy 700 cgagccaagaccaggaacatctggaatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 759
Db 621 CGAGCCAAGGACGACGACATCTTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 561
Oy 760 ctgcgtcgtatcgtgaaagggctctcctgagagcaccctggaagagagctgagtgat 819
Db 562 CTTCGCTGCATCCCTGAAAGGGCTCTTCTGAGGACCTGGAAGAGGCTGAGTGTGCA 503
Oy 820 gtacgctgcatatcagctatgaaagctgtgcaactgtacactgactgtgagagatctgagt 879
Db 502 GTACCCCTGATACAGCTATGAGAGATGGGCAACGTACTGCTGAGGAGTCTGAGT 443
Oy 880 ctgaagcgtcccaatagctatcaagaagagacatgagaggtatcatcatctgtccgtgac 939
Db 442 CTAGACGGCTCAGTAGATACATACAGAGACCATGACAGGCTACCATCATGTCTCTGCCAG 363
Oy 940 catgaatgtgcccctgtgagatgagccacagctgtgtaggcatcatcgtcgtgaatcaca 999
Db 382 CATGAATGTGCCCCTGAGATGAGACCCACAGTTGTGAGCATCAGTCCGTAAACATTCCA 323
Oy 1000 cgaagggccccaagtgtgctgcagagaaactgtggcatcagcagctggccaactgtgtgagc 1059
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Db 262 AAAGAGCCCAAAAACATCTGATGTTGACAGCGAGCTTAAGATGAGCCATTAA 209

RESULT 13
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LOCUS BE561038 60134465F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677748 5'
DEFINITION mRNA sequence.
ACCESSION BE561038
VERSION BE561038.1 GI:9804758
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1087)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: ggaabs-femail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

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CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: InCyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LHCN35 row: m column: 13
 High quality sequence stop: 723.
 Location/Qualifiers

FEATURES

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 /note="Organ: lymph; Vector: pOTB7; Site: 1: XhoI; Site_2:
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 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAAGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 270 a 291 c 345 g 181 t

ORIGIN

Query Match 59.1%; Score 657.8; DB 137; Length 1087;
 Best Local Similarity 92.4%; Prod. NO. 8e-165;

Matches 725; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

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 61 gaagaaacagcccaagatgagatgctgctggtggtacccgcaagagccagcttgt 120
 143 GAAGAAACAGCCCAAGATGAGATGATTCGCTGGGTACCCGCAAGACCCAGCTTGT 202
 121 cgcatacagagcagcagctggtggtggtggtggtggtggtggtggtggtggtggt 180
 203 CGCATACAGACGAGCAGTGTGTGCAATGTAACCTCGTACCTGGCTGCAAGTTT 262
 181 gaatcatctgctatctccacacagggaggaatctcttatactgactctctaagt 240
 263 GAAATCATCTGCTATCTCCACACAGGGAGACAGTTTCTATCTGCACTCTTAAGATT 322
 241 gggaggaagagcctcttaccagagagcctgtaacatgagcctggaagaaatgagtgagc 300
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 383 CTGGTTGTTCACTCTCTGAAGAGCTGCCCACTGTGCTCTCTCTCTCTCTCTCTCTCTCT 442
 361 gccatctgcaagcgaggaacacctcctatgctgctgctctctctctctctctctctct 420
 443 GCATCTGCAACCGGGAACCTCATGATGCTGTTGTCATCCCAAAATTTGTTGGG 502
 421 aagacccctagaacacctcagagagagtggtggtggtggtggtggtggtggtggtggtggt 480
 503 AAGACCTTAGAACCTCCGAGAGAGAGTGTGTGGAACAGCTCCCTCGCAAGAGCA 562
 481 gccacgctgcaagagaatctccgcatctgaggtctcagagatctcggggaacctcaac 540
 563 GCCACGCTGCAAGAAATTTCCCATCTGAGTTCAGGAGTATTCGGGAAACCTTCAAC 622
 541 acccggtctggaagcctgagcagcagcagaggttc-agtgcatacatctcggcaagc 599
 623 ACCCGGCTTCGGAAGCTGAGAGAGAGAGATTCAGTGCATATCTTGGCAACAC 682
 600 tggcctcagcagcagctggtggtggtggtggtggtggtggtggtggtggtggtggtggt 658

Db 683 TGGCTTCACAGCCGATGCGCTGGCAACACGCGGTGGGCAATCTTCCACACTGACGAAT 742
 659 gcatatgctgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 718
 743 GCGTGTTCGTGTGCGG-CAGGGGCGCTTGGCGCTTGAATGAGGAGCAGACCGCGGT 801

Db 719 tctgtatcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 778
 802 TCTGCGTCTGCGGGGCGGCGGCAACAGAACCGGTCCGCGCTGCTGAGAGGCTCTGA 861

Db 779 gggcc 783
 862 GGCCC 866

RESULT 14

LOCUS

AL520223 908 bp mRNA EST 13-FEB-2001
 AL520223 LTI_NFL004_NBC2 Homo sapiens CDNA clone CS0DB006Y103 5

DEFINITION
 prime, mRNA sequence.

ACCESSION
 AL520223 GI:12783716

VERSION
 AL520223.1

KEYWORDS
 EST.

SOURCE
 human.

ORGANISM
 Homo sapiens

REFERENCE
 1 (bases 1 to 908)
 Mammalia: Eutheria; Primates: Catarrhini; Hominoidea: Homo.

AUTHORS
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE
 Full-length cDNA libraries and normalization

JOURNAL
 Unpublished (2001)

COMMENT
 Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France

Email: seque@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES

source

1..908
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 /clone="CS0DB006Y103"
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 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed
 by Life Technologies. Contact: Feng Liang Life
 Technologies, a division of Invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : fliang@life.com URL :
 http://fulllength.invitrogen.com

BASE COUNT 208 a 245 c 269 g 183 t 3 others

ORIGIN

Query Match 58.8%; Score 654.6; DB 105; Length 908;
 Best Local Similarity 99.3%; Prod. NO. 5.5e-165;

Matches 676; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

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 230 GGAGAAACAGCCCAAGAGATGAGAGTATTCGCTGGTACCCGCAAGCGCACGCTTGC 289
 120 tgcataagagagcagatgtgtggtggtggtggtggtggtggtggtggtggtggtggtggt 179
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 180 tgaatcatctgctatctcaccacagggaggaagatctctgaactgcactctcaagat 239
 350 TGAATCATCTGCTATGCTCACACAGGGGACAGAGATCTTGATGACTGCACTCTTAAGAT 409

QY 240 tggagagaaagcgtgttaccagaagccttgaacatgccttgagagaagaatgaatgga 299
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Db 410 TGGAGAGAAAGCTGTTTACCAAGAGCTTGAAACATGCCCCGTGGAGAAATGAAGTGA 469
300 cctggtgttctactccttgaagagctccacatgtcttctccttggtctcaacatcg 359
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Db 470 CctGgtTgtTtCAcTcTtTAAGAGAcTGCcAcTGTGtTcTcTcTcTcTcTcTcTcTc 529
360 agccatctcgaacgaggaacacccatgatgtgtgtgttcttcaacaaattgttg 419
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Db 530 AGCCATCTGCAAGCGGAGAAACCTCATGATGCTGTGTCTTTTACCACAAATTTGTGG 589
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Db 590 GAAGACCCCTTAAGAAACCTCTCCAGAGAAAGTGTGTGGAA-CAGCTCCTCTGCAAGAGC 648
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QY 540 caccggcttcggaagccttgagacgaagacgaagatctgacatctcttgcaacagc 599
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768 TGcCTGCAAGCGATGgCTGgCAACACGgGTGgGCAAGATTCCTGCAACCTGAGAA 827
QY 660 catgtatgtctgtggcagagggccttggcgttgaaatgagacgaagacgaagcat 719
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LOCUS DEFINITION 602240467P1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:432848 5',
mRNA sequence.
ACCESSION BF971877
VERSION BF971877.1 GI:12339092
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 970)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: L1CM1189 row: f column: 17
High quality sequence stop: 724.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:432848"
/clone.lib="NIH_MGC_46"
/tissue.type="telomysarcoma cell line"
/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 244 a 262 c 296 g 168 t
ORIGIN

Query Match 58.5%; Score 651; DB 172; Length 970;
Best Local Similarity 94.8%; Pred. No. 5, 2e-164;
Matches 716; Conservative 0; Mismatches 35; Indels 4; Gaps 4;

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QY 121 gcatacagaaggacagtggtggtgcaacattgaagagctctgaacctggtccgtgca 180
230 CGCATACAGAGGACAGTGTGTGTGCAACATTAAGAGCTGACCTGCGCTGCAAGATT 289
Db 181 gaatactctatgtccacacagggagcaagatctgtgtatgtgaacctcaagatt 240
290 GAATTCATCTGTATGTCCACACAGGAGCAAGATCTTGTGATCTGACATCTCTACAA 349
QY 241 ggaagaaagcctgttaccaaaggagcttgaaatgcctcgtggaagaaatgaatgag 300
350 GGAAGAAAGCCCTGTTTACCAAGAGCTTGACATGCTGCGAAGAAATGAAGTGTGAC 409
Db 301 ctggtgttcaaccttggaagagcctgacacatgtgtctcctctgtgcttcaacatgga 360
410 CTGgTtTtCAcTcTtTAAGAGAcTGCcAcTGTGtTcTcTcTcTcTcTcTcTcTc 469
QY 361 gcatctgcagagcggaacacccatgatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
470 GCCATCTGCAAGCGGAGAAACCTCATGATGCTGTGTCTTTCACCCAAATTTGTTGG 529
Db 421 aagaccctagaacccctgcagagaagaatgtgtgtggaagacagctcctcgtgcaagaga 480
530 AAGACCTTAAGAACCTTCCAGAGAAAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589
QY 481 gccacgtgcagagaagatcccgcatctggaatcagagatcctgaggaacacctaac 540
590 G-CCAGCTGAGAGAAAGTTCCCGCATCTGAGATTACAGAGATTCGGGGAAACCTCAAC 648
Db 541 acccggttcggaagcctgcagagagagagagagagagagagagagagagagagagag 599
649 ACCGGCTTGGAAAGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 708
QY 600 tggcctgcagcagatggctgacacacccggttggcagatccttgacacctgaagaa 659
709 TGgCCTCAGAGGATGgCTGgCAACACGgGTGgGCAAGATTCCTGCAACCTGAGCA 767
Db 660 catgtatgtctgtggcagagggccttggcgttgaaatgagacgaagacgaagacat 719
768 CctGtATGCTGTGGCCA-GGGgCTGgGCGTGTGTAAGTGTGAGAGAGAGAGAGAGAGAG 826
QY 720 ctgtgacatgt 754
827 TTTGGACAGCGGAGTGTGTGACGAACCGAAA 861

Search completed: October 6, 2001, 19:05:09
Job time: 5237 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 17:39:53 ; Search time 90.47 Seconds
(without alignments)
2328.985 Million cell updates/sec

Title: US-09-601-138-12

Perfect score: 1113
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Sequence:

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94055562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
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5: /cgn2_6/prodata/1/lna/PCRNUS.COMB.seq: *
6: /cgn2_6/prodata/1/lna/Dackfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41.6	3.7	729	1	US-08-599-480-3
2	36.2	3.3	280	1	US-08-030-731A-41
3	36.2	3.3	280	1	US-08-030-731A-42
4	36.2	3.3	304	1	US-07-696-551B-12
5	35.6	3.2	7218	1	US-08-232-463-14
6	34.8	3.1	1889	2	US-08-946-241B-1
7	34.8	3.1	1889	2	US-08-946-241B-8
8	34.8	3.1	1889	3	US-09-309-053-1
9	34.8	3.1	1889	3	US-09-309-053-8
10	34.4	3.1	2502	1	US-08-073-384C-7
11	34.4	3.1	2502	1	US-08-254-359A-7
12	34.4	3.1	2502	1	US-08-483-043-7
13	34.4	3.1	2502	1	US-08-481-238-7
14	34.4	3.1	2502	2	US-08-471-066B-7
15	34.4	3.1	2502	2	US-08-484-956-7
16	34.4	3.1	2502	2	US-08-757-653-7
17	34.4	3.1	2502	2	US-08-599-491-7
18	34.4	3.1	2502	2	US-08-756-386-7
19	34.4	3.1	2502	2	US-08-823-515-7
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21	34.4	3.1	2502	3	US-08-759-038-7
22	34.4	3.1	2502	3	US-08-758-314-7
23	34.4	3.1	510	1	US-07-918-953-7
24	34.2	3.1	510	1	US-08-081-661-7
25	34.2	3.1	729	4	US-09-140-804-10
26	34.2	3.1	2793	1	US-08-209-747-1
27	34.2	3.1	2793	1	US-08-458-298-1

28	33.6	3.0	2121	4	US-09-358-683-1	Sequence 1, Appl
29	33.6	3.0	2276	1	US-08-202-389-11	Sequence 11, Appl
30	33.6	3.0	2394	4	US-08-797-358B-1	Sequence 1, Appl
31	33.6	3.0	2790	1	US-08-018-129-4	Sequence 4, Appl
32	33.6	3.0	2790	2	US-08-448-250-4	Sequence 4, Appl
33	33.4	3.0	359	3	US-08-589-028-3	Sequence 3, Appl
34	33.4	3.0	359	3	US-08-784-582-3	Sequence 3, Appl
35	33.4	3.0	359	4	US-08-785-271-3	Sequence 3, Appl
36	33.4	3.0	11219	1	US-07-642-734C-1	Sequence 1, Appl
37	33.4	3.0	11219	3	US-08-435-009A-1	Sequence 1, Appl
38	33.4	3.0	44377	2	US-08-804-227C-7	Sequence 7, Appl
39	33.4	3.0	44377	2	US-08-804-198-1	Sequence 1, Appl
40	33.2	3.0	1201	6	5252556-2	Patent No. 525256
41	33	3.0	281	1	US-07-764-655D-12	Sequence 12, Appl
42	33	3.0	281	1	US-07-764-655D-13	Sequence 13, Appl
43	33	3.0	281	6	5314646-1	Patent No. 531466
44	33	3.0	3579	1	US-08-674-168-15	Sequence 15, Appl
45	33	3.0	3579	3	US-08-985-908-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-599-480-3/C
; Sequence 3, Application US/08599480
; Patent No. 5753459
; GENERAL INFORMATION:
; APPLICANT: Blanco, David R.
; APPLICANT: Miller, James N.
; APPLICANT: Lovett, Michael A.
; APPLICANT: Champion, Cheryl I.
; APPLICANT: Tempst, Paul J.
; TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF A
; TITLE OF INVENTION: T. Pallidum RARE OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/599,480
; APPLICATION NUMBER: US/08/599,480
; FILING DATE: 23-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Learn, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: 07419/018001 (CIP of 016001)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 729 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: TROMP2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..726
; US-08-599-480-3

Query Match 3.7%; Score 41.6; DB 1; Length 729;
Best Local Similarity 47.3%; Pred. No. 0.0076;
Matches 125; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 134 acagtggtggaacaatggaagcctgcaccgctgcagctgagttgaaatcgtca 193
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QY 194 tgcacacacagggagcaagatctgtatcactctcgaagtggagagaaagcc 253
DB 368 ACCCAGCAGGAGGATCTCGTAATGCTACACACCTTACGGAATTAGTCCAGCCAG 309
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DB 188 GGGAGCCCTTGTGTGATGAACCTTG 165

RESULT 2
US-08-030-731A-41
; Sequence 41, Application US/08030731A
; Patent No. 5426036
; GENERAL INFORMATION:
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Riess, Guenther Johannes
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Walimeler, Holger
; TITLE OF INVENTION: Processes for the Preparation of Foreign
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,731A
; FILING DATE: 12-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/189,840
; FILING DATE: 03-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/430,622
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/687,610
; FILING DATE: 19-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,757
; FILING DATE: 29-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 37 14 866.4
; FILING DATE: 05-MAY-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 38 37 273.8
; FILING DATE: 03-NOV-1988

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 39 27 449.7
; FILING DATE: 19-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 12 818.0
; FILING DATE: 21-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirschner Michael K.
; REGISTRATION NUMBER: 34,851
; REFERENCE/DOCKET NUMBER: 02481-0593-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-030-731A-41

Query Match 3.3%; Score 36.2; DB 1; Length 290;
Best Local Similarity 46.6%; Pred. No. 0.19;
Matches 116; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

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QY 623 acacacgggttgagcagatcctgcacccctgaggaatgcatgtagctgtggcgagg 682
DB 80 GCTTCTTCAACACACCCAGAACCCCGGAGGAGAGACCTCAAGTGGGCAAGTGG 139
QY 683 ccttgagcgttggaagtgcgagcgaagagacatcttgagatctgtgtgtgtgtgc 742
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DB 200 AGAAGCGGCGCATCGTGAGGAGAGTCTGTACACAGCATCTGCTTACACTTGAGA 259
QY 803 gaggctgca 811
DB 260 ACTACTGCA 268

RESULT 3
US-08-030-731A-42/C
; Sequence 42, Application US/08030731A
; Patent No. 5426036
; GENERAL INFORMATION:
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Riess, Guenther Johannes
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Walimeler, Holger
; TITLE OF INVENTION: Processes for the Preparation of Foreign
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,731A
FILING DATE: 12-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/189,840
FILING DATE: 03-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/430,622
FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/687,610
FILING DATE: 19-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,757
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 37 14 866.4
FILING DATE: 05-MAY-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 38 37 273.8
FILING DATE: 03-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 39 27 449.7
FILING DATE: 19-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 818.0
FILING DATE: 21-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Kirschner Michael K.
REGISTRATION NUMBER: 34,851
REFERENCE/DOCKET NUMBER: 02481-0593-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: misc.feature
LOCATION: 5..290
OTHER INFORMATION: /note="Sequence ID No. 5426036 42 is
OTHER INFORMATION: complementary to Sequence ID No. 5426036 41 at positions
OTHER INFORMATION: 5-230 of Sequence ID No. 5426036 41."
US-08-030-731A-42

Query Match 3.3%; Score 36.2; DB 1; Length 290;
Best Local Similarity 46.6%; Pred. No. 0.19;
Matches 116; Conservative 0; Mismatches 133; Indels 0; Gaps 0;
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DB 275 ACCACACACTCTGCGGCTCCACCTAGTAGACCTCTACCTGCTGCTGCGGAGCGCAG 216
QY 623 acaacccggttggcagatcctgcaacctgaggaatgcatgtatgctgtgagcagggg 682
DB 215 CTTTCTTACACACACCAAGACCCCGGAGGAGCAGACCCCTCAGGTGAGGTGCGGAGGTG 156
QY 683 ccttggcgctggaagtgcgagcaagagacacatcttgatctgtgtggtgtgtcgc 742
DB 155 ACCTGGGCGGGGCGCTGGCGCAGCGAGCTTGAGCCCTTGGCGCGGAGGCGCTCCGTC 96
QY 743 acgagcccgagagactctgctgctgcatgctgaaaggccttctgagagcaacctggaag 802
DB 95 AATAACGGCGGATCTGTGAGAGCATGTCTGCACACAGCATCTGTCTCTTACACAGCTGAGA 36
QY 803 gaggctgca 811

DB 35 ACTACTGCA 27
RESULT 4
US-07-696-551B-12
Sequence 12 Application US/07696551B
Patent No. 5232841
GENERAL INFORMATION:
APPLICANT: Hashimoto, Tamotsu
APPLICANT: Tsujimura, Akiyoshi
APPLICANT: Ueda, Shigeo
TITLE OF INVENTION: Process for Preparing Peptide
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farrow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/PC-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/696,551B
FILING DATE: 19910509
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-122166
FILING DATE: 11-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-334575
FILING DATE: 30-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence M. Lavlin, Jr.
REGISTRATION NUMBER: 30,768
REFERENCE/DOCKET NUMBER: 2481-1070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-696-551B-12

Query Match 3.3%; Score 36.2; DB 1; Length 304;
Best Local Similarity 46.6%; Pred. No. 0.19;
Matches 116; Conservative 0; Mismatches 133; Indels 0; Gaps 0;
QY 563 agcagcagagatcattgcatcattcctgcaacagctgctgcaagcattgagctgagc 622
DB 43 ACCACACACTCTGCGGCTCCACCTAGTAGACCTCTACCTGCTGCTGCGGAGCGCAG 102
QY 623 acaacccggttggcagatcctgcaacctgaggaatgcatgtatgctgtgagcagggg 682
DB 103 CTTTCTTACACACACCAAGACCCCGGAGGAGCAGACCCCTCAGGTGAGGTGCGGAGGTG 162
QY 683 ccttggcgctggaagtgcgagcaagagacacatcttgatctgtgtggtgtgtcgc 742
DB 163 ACCTGGGCGGGGCGCTGGCGCAGCGAGCTTGAGCCCTTGGCGCGGAGGCGCTCCGTC 222
QY 743 agatgcccgagagactctgctgctgcatgctgaaaggccttctgagagcaacctggaag 802
DB 223 AGAAGCGCGGATCTGTGAGAGCATGTCTGCACACAGCATCTGTCTCTTACACAGCTGAGA 282

OY 806 gctgcagtgctccagtagcgt 827
 11111 111 11111
 DB 1314 TGTGACGCCGGCGGTGGCCAT 1293

RESULT 7
 US-08-946-241B-8/c
 : Sequence 8, Application US/08946241B
 : Patent No. 5928941
 : GENERAL INFORMATION:
 : APPLICANT: Lee, Mu-En
 : APPLICANT: MCA/Nulty, Megan M.
 : TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
 : NUMBER OF SEQUENCES: 13
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Fish & Richardson P.C.
 : STREET: 225 Franklin Street
 : CITY: Boston
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02110-2804
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/946,241B
 : FILING DATE: 07-OCT-1997
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/030,035
 : FILING DATE: 05-NOV-1996
 : APPLICATION NUMBER: 60/027,521
 : FILING DATE: 07-OCT-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Creason, Gary L.
 : REGISTRATION NUMBER: 34,310
 : REFERENCE/DOCKET NUMBER: 05433/027001
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-542-5070
 : TELEFAX: 617-542-8906
 : TELEX: 200154
 : INFORMATION FOR SEQ ID NO: 8:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1889 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: Coding Sequence
 : LOCATION: 407...1843
 : US-08-946-241B-8

Query Match 3.18; Score 34.8; DB 2; Length 1889;
 Best Local Similarity 52.88; Pred. No. 1.2;
 Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
 OY 686 tgggcgtggaagtcgagcaaggaccagacatcttgatctgtgtggtgtgtgtgacag 745
 1111 111111 111 1111 11 11 1111
 DB 1434 TGGGATGTGAAGCCGGGAGGAGGCGGACAGGTGACAGTCCCTGCTCTCAGCACT 1375
 OY 746 atcccgagactctgtctgtcatcgctgaaggagccttcctgtgaagcaccctgggaagag 805
 1111 1111 11 111 11 111 111 111 11111
 DB 1374 TCCTCAAGACCCAGGGCTGGGGTGTCTGCTGGGAGCTGCCGCCCAAGGGAAGTCG 1315
 OY 806 gctgcagtgctccagtagcgt 827
 11111 111 11111
 DB 1314 TGTGACGCCGGCGGTGGCCAT 1293

RESULT 8
 US-09-309-053-1/c

: Sequence 1, Application US/09309053
 : Patent No. 6077933
 : GENERAL INFORMATION:
 : APPLICANT: Lee, Mu-En
 : APPLICANT: MCA/Nulty, Megan M.
 : TITLE OF INVENTION: REPRESSOR KRUPPEL-LIKE FACTOR
 : NUMBER OF SEQUENCES: 13
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Fish & Richardson P.C.
 : STREET: 225 Franklin Street
 : CITY: Boston
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02110-2804
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/309,053
 : FILING DATE:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/946,241
 : FILING DATE: 07-OCT-1997
 : APPLICATION NUMBER: 60/030,035
 : FILING DATE: 05-NOV-1996
 : APPLICATION NUMBER: 60/027,521
 : FILING DATE: 07-OCT-1996
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Creason, Gary L.
 : REGISTRATION NUMBER: 34,310
 : REFERENCE/DOCKET NUMBER: 05433/027001
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-542-5070
 : TELEFAX: 617-542-8906
 : TELEX: 200154
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1889 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: Coding Sequence
 : LOCATION: 434...1843
 : US-09-309-053-1

Query Match 3.18; Score 34.8; DB 3; Length 1889;
 Best Local Similarity 52.88; Pred. No. 1.2;
 Matches 75; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
 OY 686 tgggcgtggaagtcgagcaaggaccagacatcttgatctgtgtggtgtgtgtgacag 745
 1111 111111 111 1111 11 11 1111
 DB 1434 TGGGATGTGAAGCCGGGAGGAGGCGGACAGGTGACAGTCCCTGCTCTCAGCACT 1375
 OY 746 atcccgagactctgtctgtcatcgctgaaggagccttcctgtgaagcaccctgggaagag 805
 1111 1111 11 111 11 111 111 111 1111
 DB 1374 TCCTCAAGACCCAGGGCTGGGGTGTCTGCTGGGAGCTGCCGCCCAAGGGAAGTCG 1315
 OY 806 gctgcagtgctccagtagcgt 827
 11111 111 11111
 DB 1314 TGTGACGCCGGCGGTGGCCAT 1293

RESULT 9
 US-09-309-053-8/c
 : Sequence 8, Application US/09309053
 : Patent No. 6077933
 : GENERAL INFORMATION:
 : APPLICANT: Lee, Mu-En
 : APPLICANT: MCA/Nulty, Megan M.


```

ADDRESS: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,238
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-481-238-7

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Query Match          3.1%; Score 34.4; DB 1; Length 2502;
Best Local Similarity 44.0%; Pred. No. 1.8;
Matches 128; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 491 agagaaggttcgcagatcggagtcagagatcgggggaacctcaaccggcttc 550
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1232 AGAGGCTCTCCGAAACCTNNNGCAGCCCTTGGAGGGAGAGAGCTCTTGGCTTT 1291
QY 551 ggaagctgagagcagcagagagatcagtcgcatcattcctggcaacgctggcctgagc 610
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1292 ACCAGAGAGGTGGAGAGCCCTTTCCGGGTCTGGGCCACATGAGGCCAGCGGGGTNC 1351
QY 611 gcatgggctgagcaacacgggttgaggcagatccctgcacccctgaggaatgcatgtacg 670
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1352 GGCTGGAGCTGACCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGAGAGATCCGCCGCC 1411
QY 671 tgggccaaggggccttggtggtggaagtgcgagccaaggaccagagacatcttgatctgg 730
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1412 TCGAGGAGGAGGTCTTCCGCCCTGGCGGCCACCCCTTCAACTCAACTCCCGGAGCACG 1471
QY 731 tgggtgtcgtcagatcccgagacatcgtctcgtcgtcgtcgtcgtcgtcgtcgtcgtc 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1472 TGGAAAGGCTCTTTGACGAGCTNNGGCTTCCCGCATGCGCAAGACGG 1522

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```

RESULT 14
US-08-471-066B-7
Sequence 7, Application US/08471066B
Patent No. 5837450
GENERAL INFORMATION:
APPLICANT: Dahlberg, James E.
APPLICANT: Lynamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: 5' Nucleases Derived From Thermostable
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California

```

```

COUNTRY: United States of America
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,066B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-01800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-471-066B-7

```

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Query Match          3.1%; Score 34.4; DB 2; Length 2502;
Best Local Similarity 44.0%; Pred. No. 1.8;
Matches 128; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 491 agagaaggttcgcagatcggagtcagagatcgggggaacctcaaccggcttc 550
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1232 AGAGGCTCTCCGAAACCTNNNGCAGCCCTTGGAGGGAGAGAGCTCTTGGCTTT 1291
QY 551 ggaagctgagagcagcagagagatcagtcgcatcattcctggcaacgctggcctgagc 610
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1292 ACCAGAGAGGTGGAGAGCCCTTTCCGGGTCTGGGCCACATGAGGCCAGCGGGGTNC 1351
QY 611 gcatgggctgagcaacacgggttgaggcagatccctgcacccctgaggaatgcatgtacg 670
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1352 GGCTGGAGCTGACCTACCTCCAGGCCCTNTCCCTGGAGGTGGCGAGAGATCCGCCGCC 1411
QY 671 tgggccaaggggccttggtggtggaagtgcgagccaaggaccagagacatcttgatctgg 730
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1412 TCGAGGAGGAGGTCTTCCGCCCTGGCGGCCACCCCTTCAACTCAACTCCCGGAGCACG 1471
QY 731 tgggtgtcgtcagatcccgagacatcgtctcgtcgtcgtcgtcgtcgtcgtcgtcgtc 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1472 TGGAAAGGCTCTTTGACGAGCTNNGGCTTCCCGCATGCGCAAGACGG 1522

```

```

RESULT 15
US-08-484-956-7
Sequence 7, Application US/08484956
Patent No. 5843654
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDBURG, MARY C.
APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF P53 MUTATIONS

```


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FT XX /note= "silent mutation"

PN XX MO9937325-A2.

XX XX 29-JUL-1999.

PD XX

XX XX

PF 27-JAN-1999; 99MO-DK00040.

PR 30-DEC-1998; 98DK-0001748.

PR 27-JAN-1998; 98DK-0000112.

XX XX

PA (HEME-) HEMEBIOTECH AS.

XX XX

PI Pogh J, Gellerfors P;

XX XX WPI; 1999-478987/40.

DR P-PSDB; AAY06611.

XX XX

PT Treatment of acute intermittent porphyria and other porphyric

PS diseases using an enzyme belonging to the haem biosynthetic pathway

XX XX

PS Claim 36; Page 91; 100pp; English.

XX XX

CC This is the nucleotide sequence of human PBGD clone 1.1 coding for

CC an erythropoietic expressed form of porphobilinogen desaminase

CC (PBGD, see AAY06611). PBGD catalyses the rate-limiting step of the

CC haem biosynthetic pathway. cDNA was cloned from spleen, bone

CC marrow, lymph node, lung, whole brain and adipose tissue using a

CC nested PCR strategy. 8 PBGD clones were sequenced (see AAX87630 and

CC AAX87633-36). Clone 1.1, from spleen cDNA, has 5 changes from the

CC previously published sequence but represents the most prevalent

CC wild-type allele in the population. Mutation of the PBGD gene is

CC associated with the autosomal dominant disorder acute intermittent

CC porphyria (AIP). A claimed method of treating a patient having a

CC mutation in the PBGD gene comprises using a human PBGD cDNA

CC sequence of either non-erythropoietic form (see AAX87631) or

CC erythropoietic form (especially the present sequence) according

CC to the tissue in which PBGD should be expressed, and transfection

CC of the patient with the relevant cDNA. Gene therapy treatment of

CC patients with AIP by a correction of one of the specific point

CC mutations identified as causing the disease by use of chimeraplasty

CC gene repair is also claimed. Other enzymes involved in the haem

CC biosynthetic pathway can also be used to treat various porphyrias.

XX XX

SQ Sequence 1035 BP; 250 A; 271 C; 302 G; 212 T; 0 other;

Query Match 100.0%; Score 1035; DB 20; Length 1035;

Best Local Similarity 100.0%; Pred. NO. 26-279;

Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgagagtgatcgctggtggtacccgcaagagcagctgtctgcatacagacgacagt 60

DB 1 atgagagtgatcgctggtggtacccgcaagagcagctgtctgcatacagacgacagt 60

QY 61 gtgtgtgcaacattgaagacgttcgtacccgtgagtttaattcgttaagtc 120

DB 61 gtgtgtgcaacattgaagacgttcgtacccgtgagtttaattcgttaagtc 120

QY 121 accacaggggacaagattctgatactgacactctaaattggaagagaagcgtgtt 180

DB 121 accacaggggacaagattctgatactgacactctaaattggaagagaagcgtgtt 180

QY 181 accaagagagctgaaacatcgctgagagagagatgaatgagcctgtgttcaatccttg 240

DB 181 accaagagagctgaaacatcgctgagagagagatgaatgagcctgtgttcaatccttg 240

QY 241 aaggagactgccaactgtctctcctcctggttcacacacgagacatctgcgaagcgggaa 300

DB 241 aaggagactgccaactgtctctcctcctggttcacacacgagacatctgcgaagcgggaa 300

QY 301 aaccctcagagatgctgtcttccacccaattttctggagaagccttagaaaccccg 360

DB 301 aaccctcagatgctgtcttcttccccaattttctggagaagccttagaaaccccg 360

DB 301 aaccctcagatgctgtcttcttccccaattttctggagaagccttagaaaccccg 360

QY 361 ccagagagaagatgtgtgttggaacacagctccctcgtcgaaagagacgcctgcgaagaaag 420

DB 361 ccagagagaagatgtgtgttggaacacagctccctcgtcgaaagagacgcctgcgaagaaag 420

QY 421 ttcccgatcttgagatctgagagatctgggggaaaccccaacacccgcttcggaagctg 480

DB 421 ttcccgatcttgagatctgagagatctgggggaaaccccaacacccgcttcggaagctg 480

QY 481 gacagagcaagagatctgacatcactctggaacacagctcgtcgacagcagatgggc 540

DB 481 gacagagcaagagatctgacatcactctggaacacagctcgtcgacagcagatgggc 540

QY 541 tggcacaacagggttgaggagatctcctgacaccttgagagaaatgcatgtgtgtggccag 600

DB 541 tggcacaacagggttgaggagatctcctgacaccttgagagaaatgcatgtgtgtggccag 600

QY 601 ggggcttgaggctggaagtcgagacaaagacaaagacatctggaatctgtgtgtgtg 660

DB 601 ggggcttgaggctggaagtcgagacaaagacaaagacatctggaatctgtgtgtgtg 660

QY 661 ctgcagatccgagagatctgctgctgcatctgctgaagggctcctggaagcaccgtg 720

DB 661 ctgcagatccgagagatctgctgctgcatctgctgaagggctcctggaagcaccgtg 720

QY 721 gaagagagctgcagatgtgcagtagcgtgcatcagctatgaagatgggcaactgtac 780

DB 721 gaagagagctgcagatgtgcagtagcgtgcatcagctatgaagatgggcaactgtac 780

QY 781 ctgacgtggagagatctgagatctagaacgctcagatgcatcagaagagacatgagct 840

DB 781 ctgacgtggagagatctgagatctagaacgctcagatgcatcagaagagacatgagct 840

QY 841 accatcagctcctcgtcgcaagatgaagtgctgctgaagatgacacacagctgtgaagc 900

DB 841 accatcagctcctcgtcgcaagatgaagtgctgctgaagatgacacacagctgtgaagc 900

QY 901 atcactgtcgtgaacattccacagagggccagctgtgctgcacgaacttgagacatcagc 960

DB 901 atcactgtcgtgaacattccacagagggccagctgtgctgcacgaacttgagacatcagc 960

QY 961 ctggcaactctgtctgagcaagagacaaagacaaacatcctggaatgtgacagcaatg 1020

DB 961 ctggcaactctgtctgagcaagagacaaagacaaacatcctggaatgtgacagcaatg 1020

QY 1021 aacgattgccattaa 1035

DB 1021 aacgattgccattaa 1035

RESULT 2

AAAF72848

ID AAFF72848 standard; DNA: 1035 BP.

XX XX

XX AAFF72848;

XX XX

DT 24-APR-2001 (first entry)

XX XX

DE Erythropoietic form PBGD 1.1.

XX XX

XX Heme biosynthetic pathway; gene therapy; AIP; ALA;

XX XX delta-aminolevulinic acid; deficient porphyria; ADP;

XX XX porphyria cutanea tarda; PCT; hereditary coproporphyrin; HCP;

XX XX harderoporphyria; HBP; variegate porphyria; VP;

XX XX congenital erythropoietic porphyria; CEP;

XX XX erythropoietic protoporphyria; EPP;

XX XX hepatoerythropoietic porphyria; HEP; ds.

XX XX Homo sapiens.

XX XX

XX WO200107065-A2.

PD 01-FEB-2001.
 XX 27-JUL-2000; 2000MO-DK00425.
 PF 27-JUL-1999; 99DK-0001071.
 PR 19-APR-2000; 2000DK-0000667.
 XX (HEME-) HEMEBIOTEC AS.
 PA (HEME-) HEMEBIOTEC AS.
 XX Gellerfors P, Fogh J.
 DR MPI; 2001-159639/16.
 XX Treatment or prevention of porphyria, by enzyme replacement or gene
 PT therapy for correction of mutations, particularly in the
 PT porphobilinogen deaminase gene
 PS Claim 33; Page 200; 207pp; English.
 XX The present invention relates to treatment or prevention of a
 CC disease caused by deficiency of at least one enzyme of the
 CC heme biosynthetic pathway by administering at least one catalyst,
 CC optionally combined with gene therapy of the relevant mutation.
 CC The invention is useful for treating and/or preventing AIP, ALA
 CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
 CC cutanea tarda (PCT), hereditary coproporphyria (HCP), hereditary
 CC (HBP), variegate porphyria (VP), congenital erythropoietic porphyria
 CC (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
 CC porphyria (HEP).
 XX Sequence 1035 BP; 250 A; 271 C; 302 G; 212 T; 0 other;

Query Match 100.0%; Score 1035; DB 22; Length 1035;
 Best Local Similarity 100.0%; Pred. No. 2e-279;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 atgagatgattcgcgtgggtaccgcgaagagcagctgtcgtcatcacagagacagt 60
   |||||||
DB 1 atgagagtgatcgcgtgggtaccgcgaagagcagctgtcgtcatcacagagacagt 60
   |||||||

QY 61 gtggtgcaacatgtaagcctcgtaccctgctgcgcagcttgaatactgtatgctc 120
   |||||||
DB 61 gtggtgcaacatgtaagcctcgtaccctgctgcgcagcttgaatactgtatgctc 120
   |||||||

QY 121 acccaagggaagaattccttgatctgacatcctcctaagattgagagaagaagcctgtt 180
   |||||||
DB 121 acccaagggaagaattccttgatctgacatcctcctaagattgagagaagaagcctgtt 180
   |||||||

QY 181 accaaggagcttgaaatgcccctggagagaagaatgagtgacctgtgttcatcctctt 240
   |||||||
DB 181 accaaggagcttgaaatgcccctggagagaagaatgagtgacctgtgttcatcctctt 240
   |||||||

QY 241 aaggaagcctgacatgtgcttctcctcctgctgcttaccatgagacatctgaaagcgagaa 300
   |||||||
DB 241 aaggaagcctgacatgtgcttctcctcctgctgcttaccatgagacatctgaaagcgagaa 300
   |||||||

QY 301 aacctcatgtatgtctgtcttcttcaacccaaattgtgtgggaagaacctagaacctctg 360
   |||||||
DB 301 aacctcatgtatgtctgtcttcttcaacccaaattgtgtgggaagaacctagaacctctg 360
   |||||||

QY 361 ccaagagaagatgtgtgtgaggaaccagctccctctgagaagagcagccagctcgaagaaga 420
   |||||||
DB 361 ccaagagaagatgtgtgtgaggaaccagctccctctgagaagagcagccagctcgaagaaga 420
   |||||||

QY 421 ttcccgatcttgaggttcaagagatctcggggaaacctaaaccggcttcgggaagctg 480
   |||||||
DB 421 ttcccgatcttgaggttcaagagatctcggggaaacctaaaccggcttcgggaagctg 480
   |||||||

QY 481 gacgagcagcagagatcagtgccatcatcctctgcaacagctgacctcagcgcatggc 540
   |||||||
DB 481 gacgagcagcagagatcagtgccatcatcctctgcaacagctgacctcagcgcatggc 540
   |||||||

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QY 541 tggcaaacccgggttgaggagatcctgcacccctgagaagaatcatgatatctctgtggccag 600
   |||||||
DB 541 tggcaaacccgggttgaggagatcctgcacccctgagaagaatcatgatatctctgtggccag 600
   |||||||

QY 601 gggaccttgagcgtggaagtgcagagcagaagagacagacatctgatactcgtgtgtgtg 660
   |||||||
DB 601 gggaccttgagcgtggaagtgcagagcagaagagacagacatctgatactcgtgtgtgtg 660
   |||||||

QY 661 ctgcagatccccaagactctgtctctgctgcatcgtctgaagaagcctcctcgaaggacctg 720
   |||||||
DB 661 ctgcagatccccaagactctgtctctgctgcatcgtctgaagaagcctcctcgaaggacctg 720
   |||||||

QY 721 gaagagagctgcagctgtgcagtagccgtgcatatagatcatagaagaatgagcaactgtac 780
   |||||||
DB 721 gaagagagctgcagctgtgcagtagccgtgcatatagatcatagaagaatgagcaactgtac 780
   |||||||

QY 781 ctgactgagaagatctggagatcgaagcagctgaagatagacatacaagaagacatcgaagct 840
   |||||||
DB 781 ctgactgagaagatctggagatcgaagcagctgaagatagacatacaagaagacatcgaagct 840
   |||||||

QY 841 accatcatgtccctgcccagcatgagaatggccctgagagatgacacacagttgttaggc 900
   |||||||
DB 841 accatcatgtccctgcccagcatgagaatggccctgagagatgacacacagttgttaggc 900
   |||||||

QY 901 atcactgtgttaactcttcacagagggcccaagttggtgtcccaagacttggcatagc 960
   |||||||
DB 901 atcactgtgttaactcttcacagagggcccaagttggtgtcccaagacttggcatagc 960
   |||||||

QY 961 ctggcccaactgtgtctgtagcagaagagcacaacacatcctgtgattgttcacggcgaattg 1020
   |||||||
DB 961 ctggcccaactgtgtctgtagcagaagagcacaacacatcctgtgattgttcacggcgaattg 1020
   |||||||

QY 1021 aacgatgccattaa 1035
   |||||||
DB 1021 aacgatgccattaa 1035
   |||||||

RESULT 3
AXX87631
ID AAX87631 standard; cDNA; 1113 BP.
XX
XX AAX87631:
AC 26-OCT-1999 (first entry)
DT
XX
XX Human non-erythroid porphobilinogen deaminase clone 1.1.1.
DE
XX
XX Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW porphyria cutanea tarda; hereditary coproporphyria;
KW hereditary porphyria; congenital erythropoietic porphyria;
KW variegate porphyria; erythropoietic protoporphyria;
KW hepatoerythropoietic porphyria; acute intermittent porphyria;
KW gene therapy; enzyme replacement therapy; ds.
XX
XX Homo sapiens.
OS
XX
XX W09937325-A2.
PN
XX
XX 29-JUL-1999.
PD
XX
XX 27-JAN-1999; 99MO-DK00040.
PF
XX
XX 30-DEC-1998; 98DK-0001748.
PR
XX
XX 27-JAN-1998; 98DK-0000112.
XX
XX (HEME-) HEMEBIOTEC AS.
PA
XX
XX Fogh J, Gellerfors P;
PI
XX
XX MPI; 1999-478987/40.
DR
XX
XX Treatment of acute intermittent porphyria and other porphyritic
PT diseases using an enzyme belonging to the haem biosynthetic pathway

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Db 131 atgagagtgatctcgctgggtaaccgcaagagccagctgtctgcatacagagagcagt 190
Qy 61 gtggtagcaaacattgaaagcctctgtmcccttgcctgcagcttgaatacattgctatgcc 120
Db 191 gtggtagcaaacattgaaagcctctgtmcccttgcctgcagcttgaatacattgctatgcc 250
Qy 121 accaagagggaacaaagattcttgaatacctctcctaagagattggaagaaagcctttc 180
Db 251 accaagagggaacaaagattcttgaatacctctcctaagagattggaagaaagcctttc 310
Qy 181 accaagaggcttgaacatgcctctggaagaaatgaaagagccggtgtgttcaactcttc 240
Db 311 accaagaggcttgaacatgcctctggaagaaatgaaagagccggtgtgttcaactcttc 370
Qy 241 aaggaacctgcacatgtcttccctcctcctgtgtctaacatctggaagccatctgaaagcgga 300
Db 371 aaggaacctgcacatgtcttccctcctcctgtgtctaacatctggaagccatctgaaagcgga 430
Qy 301 aacctcatatgattctgtcttccaccaaataattgttggaaagaccctagaagaccctg 360
Db 431 aacctcatatgattctgtcttccaccaaataattgttggaaagaccctagaagaccctg 490
Qy 361 ccagagaagaagctgtgtgtggaacacagctctccctgcgaagagacagccctgcagagaag 420
Db 491 ccagagaagaagctgtgtgtggaacacagctctccctgcgaagagacagccctgcagagaag 550
Qy 421 ttcctgcattctgagcttcagagagattctcgaggaaaccccaacacccgctctcgaaagctg 480
Db 551 ttcctgcattctgagcttcagagagattctcgaggaaaccccaacacccgctctcgaaagctg 610
Qy 481 gacagagacagagagattctgagcttccatctcctggaacagctgtgcctgcagccatctggagc 540
Db 611 gacagagacagagagattctgagcttccatctcctggaacagctgtgcctgcagccatctggagc 670
Qy 541 tggcaacaaccgggttctggcagatctctgcacccctggaagaaatgcatgatactgtctgggcccag 600
Db 671 tggcaacaaccgggttctggcagatctctgcacccctggaagaaatgcatgatactgtctgggcccag 730
Qy 601 ggggaccttgggcttgggaagtggcagaacaggaacacatctgtgctctggctgggctgtg 660
Db 731 ggggaccttgggcttgggaagtggcagaacaggaacacatctgtgctctggctgggctgtg 790
Qy 661 ctgcacagatcccgagatctgtctgtctgcatactgcctgaaaggccctctcctgaagccactg 720
Db 791 ctgcacagatcccgagatctgtctgtctgcatactgcctgaaaggccctctcctgaagccactg 850
Qy 721 gaaaggagctgtgcagctgtgcagctgtagccgtgcatagactctgaaagagatgggcaactgtac 780
Db 851 gaaaggagctgtgcagctgtgcagctgtagccgtgcatagactctgaaagagatgggcaactgtac 910
Qy 781 ctgactggaagagctctggaagctctgaagcctcagataagcatatacagaagacatctgacgct 840
Db 911 ctgactggaagagctctggaagctctgaagcctcagataagcatatacagaagacatctgacgct 970
Qy 841 accatccatgctccctgcagcaatgaagaatggccctggaagatgaaccacagcttgggaagc 900
Db 971 accatccatgctccctgcagcaatgaagaatggccctggaagatgaaccacagcttgggaagc 1030
Qy 901 atcacgtctgtgaatacatctcagaagagcccaagcttggctgcagagaacttgggcatcagc 960
Db 1031 atcacgtctgtgaatacatctcagaagagcccaagcttggctgcagagaacttgggcatcagc 1090
Qy 961 ctggcacaacttctgtctgagcaagaagacaaacatacctctgagatctgcacagccatgtg 1020
Db 1091 ctggcacaacttctgtctgagcaagaagacaaacatacctctgagatctgcacagccatgtg 1150
Qy 1021 aacgagagcccatctaa 1035
Db 1151 aacgagagcccatctaa 1165

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RESULT 6
AAx87639/c

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ID AXx87639 standard; cDNA: 3988 BP.
XX
AC AXx87639;
XX
DT 26-OCT-1999 (first entry)
XX
DE Human porphobilinogen deaminase clone 1.1 in pBluescript SK-.
XX
KW porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW porphyria cutanea tarda; hereditary coproporphyria;
KW hemoerythropoietic porphyria; congenital erythropoietic porphyria;
KW variegate porphyria; erythropoietic protoporphyria;
KW hemoerythropoietic porphyria; acute intermittent porphyria;
KW gene therapy; enzyme replacement therapy; plasmid pBluescript SK-;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS complement (1730..696)
FT /tag= a
XX
XX MO9937325-A2.
XX
PD 29-JUL-1999.
XX
PF 27-JAN-1999: 99WO-DK00040.
XX
PR 30-DEC-1998: 98DK-0001748.
PR 27-JAN-1998: 98DK-0000112.
XX
PA (HEME-) HEMEBIOTECH AS.
XX
PI Fogh J, Gelferfors P;
XX
DR WPI: 1999-478987/40.
DR P-PSDB: AAY06611.
XX
PT Treatment of acute intermittent porphyria and other porphyric
PT diseases using an enzyme belonging to the haem biosynthetic pathway
XX
PS Disclosure: Fig 9a-x; 100pp; English.
XX
XX This is the nucleotide sequence of human PBGD clone 1.1 (see
XX AXx87639) in plasmid Bluescript SK-, allowing recombinant expression
XX of porphobilinogen deaminase (PBGD, see AAY06611). PBGD catalyses
XX the rate-limiting step of the haem biosynthetic pathway. Mutation
XX of the PBGD gene is associated with the autosomal dominant disorder
XX acute intermittent porphyria (AIP). A claimed method of treating a
XX patient having a mutation in the PBGD gene comprises using a human
XX PBGD cDNA sequence of either non-erythropoietic form (see AXx87631)
XX or erythropoietic form (especially clone 1.1 cDNA), according to the
XX tissue in which PBGD should be expressed, and transfection of the
XX patient with the relevant cDNA. Gene therapy treatment of patients
XX with AIP by a correction of one of the specific point mutations
XX identified as causing the disease by use of chimera-plasty gene
XX repair is also claimed.
XX
SQ Sequence 3988 BP: 918 A; 1056 C; 1000 G; 1014 T; 0 other:

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Query Match 100.0%; Score 1035; Dn 20; Length 3988;
Best Local Similarity 100.0%; Pred. No. 3,7e-279;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 atgagagtgatctgtgtgtgacccgaagagccagctgtctgcatacagaagagcagt 60
Db 1730 atgagagtgatctgtgtgtgacccgaagagccagctgtctgcatacagaagagcagt 1671
Qy 61 gtggtagcaaacattgaaagcctctgtmcccttgcctgcagcttgaatacattgctatgcc 120
Db 1670 gtggtagcaaacattgaaagcctctgtmcccttgcctgcagcttgaatacattgctatgcc 1611

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121 accacagggagaagatctctgaactcctctaagattgagagaagacgtttc 180
1610 ACCACAGGGGACAGATTCTTGATGACTGCACTCTTAATATGGAGAAAAAGCCTGTTT 1551
181 accaagagcttgacacatgcccggagaaatgaagtgaacctgtgttccactcttg 240
1550 ACCAAGAGGCTGTAACATGCCCTGGAGAAATGAAGTGAAGCTGTGTTCTACTCCTTG 1491
241 aaggaactgcccactgtgtctctcctctgcttcaaccatcgaagcactgtcaagcgagaa 300
1490 AAGGACTGCCCACTGTGCTTCTCTGCTTCACCATGCGACCATCTGCACCGGAA 1431
301 aacctcaatgtctgtctgtcttcaacccaattgtgtgaaagacctagaaccttg 360
1430 AACCTCATATGCTGTGTGCTTTCACCAAAATTTGTTGGAGAACCTTGAAACCTTG 1371
361 ccagaagaagatgtgtgtggaaccagctccctcgcgaagaagaccctgcagagaag 420
1370 CCAGAAGAAGATGTGTGGGAAACACAGCTCCTGCGAAGACGCCACCTGCAGAGAAAG 1311
421 tcccgacactgaggttcagagatttcggggaaacctcaaccggccttcggaagctg 480
1310 TTCCCGCATCTGGAGTTCAAGAGTATTCCGGGAAACCTCAACCCGGCTTCGGAAGCTG 1251
481 gaagagcagcaggaagttcagttgccatcaactcgtgcaacagctgcccgcagcgaatggc 540
1250 GACGACGACGAGGAGTTCACTGCAATCCTGCGCAACAGCTGCCCTCAGCGCATGGCG 1191
541 tggacaacacgggttggcagatcctgcacccctgaaagaaatgcatglatgtctgagcag 600
1190 TGGCAACACGGGTTGGGAGATCCTGCAACCTGAGAGATGATGATGCTGGGCGAG 1131
601 ggggctctgggctgaggaatgagcgaagacgaagacgaatcttgatctgtgtgtgtg 660
1130 GGGGCTTGGGCTGGAAGTGCAGAGCCAGACGACATCTTGATCTGGTGGCTGTG 1071
661 ctgacgacatcccgagactctgtctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 720
1070 CTGACGATCCCGAGACTCTGCTCTGCTGATGCTGAGAAAGGCTCTCTGAGGACCTG 1011
721 gaaggaagctgcaatgtgcgaagtcgagtcgaatgacgataagaatgaggaactgtac 780
1010 GAAGGAGCTGCAATGTGCCAGTACGCGTGCATACAGCTATGAGAGATGGCAACTGTAC 951
781 ctgactggaagagatctgagatctcagaacggtcagatagacatacaagaagacatgcaagct 840
950 CTGACTGAGAGAGTCTGAGATCTAGACGGCTCAGATAGCATACAGAGACCATGAGGCT 891
841 accatcactgctcctgctccagcagatgaagatgagccctgaaagatgagccagtgtgtgagc 900
890 ACCATCTGCTCCTGCTCCAGCATGAGATGCGCTGAGAGATGACCCACAGTGTGTAGCG 831
901 atcactgtctgaacatcaccagagagcccaagtlgtgtcgtcccaagaaacttgagcagc 960
830 ATCACTGCTCTAATCTCCACGAGGCGCCCACTTGCTGCCCAAGACTTGGCATCAGC 771
961 ctggcgaactgtgtgtgagcgaagagcgaagaaacatctctgattgtgtgcaggaactg 1020
770 CTGGCAACTGTGTGTGAGCAAAAGAGCCAAAAACATCTCTGATGTTGACGGCAATTG 711
1021 aacgattgccatcaa 1035
710 AACGATGCCATTA 696

RESULT 7
AAF72857/c
ID AAF72857 standard; DNA: 3988 BP.
AC AAF72857;
XX AAF72857;
XX 24-APR-2001 (first entry)

+ + 15 indel
from 1 to 1730 indel

DE PGDB DNA.
XX Heme biosynthetic pathway: gene therapy; AIP; ALA;
KM delta-aminolevulinic acid; deficient porphyria; ADP;
KM porphyria cutanea tarda; PCT; hereditary coproporphyrin; HCP;
KM henderoporphyrin; HDP; variegate porphyria; VP;
KM congenital erythropoietic porphyria; CEP;
KM erythropoietic protoporphyria; EPP;
KM hepatoerythropoietic porphyria; HEP; ds.
OS Homo sapiens.
PN MO200107065-A2.
PN 01-FEB-2001.
XX 27-JUL-2000; 2000WD-DK00425.
PF 27-JUL-1999; 99DK-0001071.
PR 19-APR-2000; 2000DK-0000667.
XX (HEME-) HEMEBIOTECH AS.
XX Gellerfors P, Fogh J;
PI WPI; 2001-159639/16.
XX Treatment or prevention of porphyria, by enzyme replacement or gene
PT therapy for correction of mutations, particularly in the
PT porphobilinogen deaminase gene
XX Disclosure; Page 203-205; 207pp; English.
XX The present invention relates to treatment or prevention of a
CC disease caused by deficiency of at least one enzyme of the
CC heme biosynthetic pathway by administering at least one catalyst,
CC optionally combined with gene therapy of the relevant mutation.
CC The invention is useful for treating and/or preventing AIP, ALA
CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC cutanea tarda (PCT), hereditary coproporphyrin (HCP), henderoporphyrin
CC (HDP), variegate porphyria (VP), congenital erythropoietic porphyria
CC (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic
CC porphyria (HEP).
XX
SQ Sequence 3988 BP; 918 A; 1056 C; 1000 G; 1014 T; 0 other;
Query Match 100.0%; Score 1035; DB 22; Length 3988;
Best Local Similarity 100.0%; Pred. No. 3.7e-279;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atgagagtgatctcgctgggtlacccggaagagcagctgtctcgacatacagaagcagcagt 60
DB 1730 ATGAGAGTGATTCGCGTGGTACCCGCAAGAGCCAGCTTGCTGCATACAGACGAGT 1671
QY 61 gttgtgcaaatgaaagctgtgacccctgagctgagctgagctgagctgagctgagctgagc 120
DB 1670 GTTGTGCAAAATTTGAAAGCTCTGACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1611
QY 121 accacagggagaagatcttgatcgaactcctctaagattgagagaagacgtttc 180
DB 1610 ACCACAGGGGACAGATTCTTGATGACTGCACTCTTAATATGGAGAAAAAGCCTGTTT 1551
QY 181 accaagagcttgacacatgcccggagaaatgaagtgaacctgtgttccactcttg 240
DB 1550 ACCAAGAGGCTGTAACATGCCCTGGAGAAATGAAGTGAAGCTGTGTTCTACTCCTTG 1491
QY 241 aaggaactgcccactgtgtctctcctctgcttcaaccatcgaagcactgtcaagcgagaa 300
DB 1490 AAGGACTGCCCACTGTGCTTCTCTGCTTCACCATGCGACCATCTGCACCGGAA 1431
QY 301 aacctcaatgtctgtctgtcttcaacccaattgtgtgaaagacctagaaccttg 360
DB 1430 AACCTCATATGCTGTGTGCTTTCACCAAAATTTGTTGGAGAACCTTGAAACCTTG 1371

Db 1430 AACCTCATGATCCTGTTGTTGTTTACCCAAATTTGTTGGAGAACCTTAGAAGCCCTG 1371
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 Db 1370 CCAAGAGAAAGTGTGTGGTGGAGAACCTCCCTGGCCAAAGAGACAGCCAGCTGCAGAGAAAG 1311
 QY 421 ttccgcacatctgagatcagagagatctcgaggaaaccccaacaccgagcttcggaagctg 480
 Db 1310 TTCCCGCATCTGCAGTTCCAGAGACTATTCGGGGAAACCTCAACACCCGGCTTCGGAACCTG 1251
 QY 481 gacagagcagcagagatcagtcagtcacatcctcggaagagcttgccgcagcagctgagc 540
 Db 1250 GACAGACAGCAGAGAGTTCAAGTGCATATCCCGCAAGAGCTGGCCCTGCAGAGCAGTGGCC 1191
 QY 541 tggcacaacacgggtctggcagagatcctgcacccctgaggaatgcatatgctgtgagccag 600
 Db 1190 TGGCACAACGGGTTGGGAGATCTCCGACCTCGAGAAATCATGTAATGCTGTGGGCGAG 1131
 QY 601 ggggacctggagctggaaatgacagcacaagagacagacatcctggaatcctgagtgagtg 660
 Db 1130 GGGGCTTGGGCTGGAGATCGCAGCAAGGACAGACATCTTGGAATCTGTGGGTGTG 1071
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 Db 1070 CTGACACATCCCGAGACTGTGCTTGCCTGCATCCGCTGAAAGGGCCTTCTGAGGCGACCTG 1011
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 QY 961 ctggcgaactctgtcgagcagaagagcacaacacatcctgagatgctgacagcgcaatc 1020
 Db 770 CTGGCAACATTTGCTGTGAGCAAGAGCCAAAACATCTCGATGTGACAGCGCAATTG 711
 QY 1021 aacgagcagcatcaa 1035
 Db 710 AACGATGCCCATTTAA 696
 RESULT 8
 AAX87632 standard; cDNA; 1035 BP.
 ID AAX87632;
 AC AAX87632;
 XX 26-OCT-1999 (first entry)
 DT 26-OCT-1999 (first entry)
 XX Human porphobilinogen deaminase clone 1.3.
 DE Human porphobilinogen deaminase clone 1.3.
 XX Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
 KM porphyria cutanea tarda; hereditary coproporphyrria;
 KM heridroporphyrria; congenital erythropoietic porphyria;
 KM varilegata porphyria; erythropoietic protoporphyria;
 KM hepaetoerythropoietic porphyria; acute intermittent porphyria;
 KM gene therapy; enzyme replacement therapy; ds.
 XX Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH variation replace(513,A)
 FT /tag= a

FT /note= "silent mutation"
 FT replace(555,A)
 FT /tag= b
 FT /note= "silent mutation"
 FT replace(995,C)
 FT /tag= c
 FT /note= "Asn to Thr substitution"
 FT replace(1017,G)
 FT /tag= d
 FT /note= "silent mutation"
 FT replace(1018,C)
 FT /tag= e
 FT /note= "silent mutation"
 FT replace(1020,T)
 FT /tag= f
 FT /note= "silent mutation"

PN M09937325-A2.

PD 29-JUL-1999.

PP 27-JAN-1999; 99WO-DK00040.

PR 30-DEC-1998; 98DK-0001748.

PR 27-JAN-1998; 98DK-0000112.

PA (HEME-) HEMEBIOTECH AS.

PI Fogh J, Gellerafors P;

DR WPI; 1999-478987/40.

PT Treatment of acute intermittent porphyria and other porphyric
 PT diseases using an enzyme belonging to the haem biosynthetic pathway
 PS Disclosure; Page 92; 100pp; English.

XX This is the nucleotide sequence of human PBGD clone 1.3 coding for
 CC an erythropoietic expressed form of porphobilinogen deaminase (PBGD).
 CC This enzyme catalyses the third, rate-limiting step of the haem
 CC biosynthetic pathway. PBGD was cloned from spleen, bone marrow,
 CC lymph node, lung, whole brain and adipose tissue cDNA using a
 CC nested PCR strategy. 8 PBGD clones were sequenced (see AAX87630 and
 CC AAX87632-38). Clone 1.3, from spleen cDNA, has 6 changes from the
 CC previously published sequence. Clone 1.1 (see AAX87630) represents
 CC the most prevalent 'wild-type' allele in the population. Mutation
 CC of the PBGD gene is associated with the autosomal dominant disorder
 CC acute intermittent porphyria (AIP). A claimed method of treating a
 CC patient having a mutation in the PBGD gene comprises using a human
 CC PBGD cDNA sequence of either non-erythropoietic form (see AAX87631)
 CC or erythropoietic form (especially clone 1.1 cDNA), according
 CC to the tissue in which PBGD should be expressed, and transfection
 CC of the patient with the relevant cDNA. Gene therapy treatment of
 CC patients with AIP by a correction of one of the specific point
 CC mutations identified as causing the disease by use of chimera-plasty
 CC gene repair is also claimed. Other enzymes involved in the haem
 CC biosynthetic pathway can also be used to treat various porphyrias.

Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;

Query Match 99.8%; Score 1033.4; DB 20; Length 1035;
 Best Local Similarity 99.9%; Pred. No. 5; e-379;
 Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atagaagatgattcgcgttggtacccgacagagccagctgctgcatacagacggaagct 60
 Db 1 atgagagtgatcgcgttggtacccgacagagccagctgctgcatacagacggaagct 60
 QY 61 gtgggtgcaacttgaaagcctgtgacccctgagctgagcttgaatcatctatgtcc 120
 Db 61 gtgggtgcaacttgaaagcctgtgacccctgagctgagcttgaatcatctatgtcc 120

OY	121	accacagaggagacaaagattctgtgtactgtacactctcaagattgaggagaaaaagcctgttt	180
Db	121	accacaaaggagacaaagatctctgtactgtacactctctcaaaattgtgaggaaaaagcctgttt	180
OY	181	accacaaagagctctgaacatgctcctgtagaaagaaatgaaatgaaactgtgtcttcaactcttg	240
Db	181	accacaaagagctctgaacatgctcctgtagaaagaaatgaaatgaaactgtgtcttcaactcttg	240
OY	241	aaggagactctgcccactgtgtctctctctctgtcttcacatcagatggagccactctgcaagcgggaa	300
Db	241	aaggagactctgcccactgtgtctctctctctctgtcttcacatcagatggagccactctgcaagcgggaa	300
OY	301	aacctcatgacgtcgtgtgtcttcttccacccaataattgtttgtagaagacctcgaanaaccttg	360
Db	301	aacctcatgacgtcgtgtgtcttcttccacccaataattgtttgtagaagacctcgaanaaccttg	360
OY	361	ccaaagagaaagagctgtgtgtgtgggaaacaaacagctccctgtagaaagagagccacagctgcagaagaaag	420
Db	361	ccaaagagaaagagctgtgtgtgtgggaaacaaacagctccctgtagaaagagagccacagctgcagaagaaag	420
OY	421	ttcccgagatcttgagattctcaagagatattctcggtgggaaaaactcaaacaccggtcttcggagaactg	480
Db	421	ttcccgagatcttgagattctcaagagatattctcggtgggaaaaactcaaacaccggtcttcggagaactg	480
OY	481	gagcagagagagagagattccaaatgtgcatactccctggacaaacagctgagcctctcagcagatgggc	540
Db	481	gagcagagagagagagattccaaatgtgcatactccctggacaaacagctgagcctctcagcagatgggc	540
OY	541	ttgacacaaaccgggtcttgagcagatctcctgacaccccttgaaagtcaatgtcatgtctgtgtagcag	600
Db	541	ttgacacaaaccgggtcttgagcagatctcctgacaccccttgaaagtcaatgtcatgtctgtgtagcag	600
OY	601	ggggccctctggagcctgtagagagctgtagcagagacaaagaaacacagagacattctgacctgtgtgtgtg	660
Db	601	ggggccctctggagcctgtagagagctgtagcagagacaaagaaacacagagacattctgacctgtgtgtgtg	660
OY	661	ctgcagagatcccagagactctgtctctgctgcatactgcctgtgaaggagcctctcagagacactg	720
Db	661	ctgcagagatcccagagactctgtctctgctgcatactgcctgtgaaggagcctctctcagagacactg	720
OY	721	gaaagagagagctgcagatgtgtagcagctgagccgtgcatatacagctatagaagatgtagcagacctgac	780
Db	721	gaaagagagagctgcagatgtgtagcagctgagccgtgcatatacagctatagaagatgtagcagacactgac	780
OY	781	ctgagctctgagagagatctctggaattctaaagacggtctcaagatacaagaagaaacctgtgaagct	840
Db	781	ctgagctctgagagagatctctggaattctaaagacggtctcaagatacaagaagaaacctgtgaagct	840
OY	841	accatccatgtccctctgcacccagcatgaagaatgagccctgaaagatgaacccaacagtctgtgtaacg	900
Db	841	accatccatgtccctctgcacccagcatgaagaatgagccctgaaagatgaacccaacagtctgtgtaacg	900
OY	901	atcacatctctgttaaatcttccacagagagagcccccagttgtgtccccaagaacttgggtcatcagc	960
Db	901	atcacatctctgttaaatcttccacagagagagcccccagttgtgtccccaagaacttgggtcatcagc	960
OY	961	ctggcccaactgtgtgtctgtagcaagaagagcccaaaaacatccttgatgttgcacagcaattg	1020
Db	961	ctggcccaactgtgtgtctgtagcaagaagagcccaaaaacatccttgatgttgcacagcaattg	1020
OY	1021	aacgatagccattaa	1035
Db	1021	aacgatagccattaa	1035
RESULT 9			
AAx87633			
ID	AAx87633 standard; cDNA; 1035 BP.		
XX	AAx87633:		
XX	26-Oct-1999 (first entry)		
XX			

XX	Human porphobilinogen deaminase clone 2.1.
KM	Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
KW	porphyria cutanea tarda; hereditary coproporphyria;
RN	harderoporphyria; congenital erythropoietic porphyria;
KV	variegata porphyria; erythropoietic protoporphyria;
RM	hepatoerythropoietic porphyria; acute intermittent porphyria;
XK	gene therapy; enzyme replacement therapy; ds.
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	variation replace(513,A)
FT	/tag- a
FT	/note= "silent mutation"
FT	variation replace(555,A)
FT	/tag- b
FT	/note= "silent mutation"
FT	variation replace(995,C)
FT	/tag- c
FT	/note= "asn to Thr substitution"
FT	variation replace(1017,G)
FT	/tag- d
FT	/note= "silent mutation"
FT	variation replace(1018,C)
FT	/tag- e
FT	/note= "silent mutation"
FT	variation replace(1020,T)
FT	/tag- f
FT	/note= "silent mutation"
PN	MO99373325-A2.
PD	29-JUL-1999.
XX	
PF	27-JAN-1999; 99NC-DK00040.
PR	30-DEC-1998; 98DK-0001748.
PR	27-JAN-1998; 98DK-0000112.
PA	(HEME-) HEMBIOTECB AS.
PI	Fogh J, Gellerfors P:
DR	WPI: 1999-478987/40.
PT	Treatment of acute intermittent porphyria and other porphyric
PS	diseases using an enzyme belonging to the haem biosynthetic pathway
XX	
PS	Disclosure; Page 92-93; 100pp; English.
CC	This is the nucleotide sequence of human PBGD clone 2.1 coding for
CC	an erythropoietic expressed form of porphobilinogen deaminase (PBGD).
CC	This enzyme catalyses the third, rate-limiting step of the haem
CC	biosynthetic pathway. PBGD was cloned from spleen, bone marrow,
CC	lymph node, lung, whole brain and adipose tissue cDNA using a
CC	nested PCR strategy. 8 PBGD clones were sequenced (see AAX87630 and
CC	AAX87632-38). Clone 2.1, from bone marrow cDNA, has 6 changes from the
CC	previously published sequence. Clone 1.1 (see AAX87630) represents
CC	the most prevalent wild-type allele in the population. Mutation
CC	of the PBGD gene is associated with the autosomal dominant disorder
CC	acute intermittent porphyria (AIP). A claimed method of treating a
CC	patient having a mutation in the PBGD gene comprises using a human
CC	PBGD cDNA sequence of either non-erythropoietic form (see AAX87631)
CC	or erythropoietic form (especially clone 1.1 cDNA), according
CC	to the tissue in which PBGD should be expressed, and transfection
CC	of the patient with the relevant cDNA. Gene therapy treatment of
CC	patients with AIP by a correction of one of the specific point
CC	mutations identified as causing the disease by use of chimera-plasty
CC	gene repair is also claimed. Other enzymes involved in the haem
CC	biosynthetic pathway can also be used to treat various porphyrias.
XX	
SQ	Sequence 1035 BP: 250 A: 271 C: 303 G: 211 T: 0 other:

Query Match 99.8%; Score 1033.4; DB 20; Length 1035;
 Best Local Similarity 99.9%; Pred. No. 5,7e-279;
 Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atgagagtgatcgcgtggtgtaaccgcaagagccagctctgcgcatacagccgacagt 60
 Db 1 atgagagtgatcgcgtggtgtaaccgcaagagccagctctgcgcatacagccgacagt 60
 QY 61 gtgtgtgcaacattgaaagccctcgtaaccctgctgacgtttgaatcatctgtatgtcc 120
 Db 61 gtgtgtgcaacattgaaagccctcgtaaccctgctgacgtttgaatcatctgtatgtcc 120
 QY 121 accacagggagacaagatcttgatctgacatctcctaagaatgagaaacccgtctt 180
 Db 121 accacagggagacaagatcttgatctgacatctcctaagaatgagaaacccgtctt 180
 QY 181 accaagaagcttgaaacagccctgagagaagaataagtgaaactggtttcactctctg 240
 Db 181 accaagaagcttgaaacagccctgagagaagaataagtgaaactggtttcactctctg 240
 QY 241 aaggaacctgcacacgtctctctcctcctcctcctcctcctcctcctcctcctcct 300
 Db 241 aaggaacctgcacacgtctctcctcctcctcctcctcctcctcctcctcctcctcct 300
 QY 301 aaccctcatgacgtcgttctcttcaaccacaatttctgagaaagccctlaagaacccgt 360
 Db 301 aaccctcatgacgtcgttctcttcaaccacaatttctgagaaagccctlaagaacccgt 360
 QY 361 ccagagagaagatgt 420
 Db 361 ccagagagaagatgt 420
 QY 421 ttcgccatctgagatctcagagatctcagagaaactcacaaccccggtctcgaaagctg 480
 Db 421 ttcgccatctgagatctcagagatctcagagaaactcacaaccccggtctcgaaagctg 480
 QY 481 gacagagcagcagagagatctcagatctcagatctcagatctcagatctcagatctg 540
 Db 481 gacagagcagcagagagatctcagatctcagatctcagatctcagatctcagatctg 540
 QY 541 tggcacaacacgggtctgagagatctcagatctcagatctcagatctcagatctcagat 600
 Db 541 tggcacaacacgggtctgagagatctcagatctcagatctcagatctcagatctcagat 600
 QY 601 gggagccttgagagtgagagtgagagtgagagtgagagtgagagtgagagtgagagtg 660
 Db 601 gggagccttgagagtgagagtgagagtgagagtgagagtgagagtgagagtgagagtg 660
 QY 661 ctgcaacgataccgagacatctgctgcgtcagatctgtaaaagggcctctcgagacacctg 720
 Db 661 ctgcaacgataccgagacatctgctgcgtcagatctgtaaaagggcctctcgagacacctg 720
 QY 721 gaaagagaggtctgagagtgagagtgagagtgagagtgagagtgagagtgagagtgag 780
 Db 721 gaaagagaggtctgagagtgagagtgagagtgagagtgagagtgagagtgagagtgag 780
 QY 781 ctgacttgagagtgagagtgagagtgagagtgagagtgagagtgagagtgagagtgag 840
 Db 781 ctgacttgagagtgagagtgagagtgagagtgagagtgagagtgagagtgagagtgag 840
 QY 841 accatcatctgctcgcgcacagatgaaagtgagagtgagagtgagagtgagagtgagagtg 900
 Db 841 accatcatctgctcgcgcacagatgaaagtgagagtgagagtgagagtgagagtgagagtg 900
 QY 901 atcactgctctgtaacatctcagagagggcccaagtctgagagtgagagtgagagtgagag 960
 Db 901 atcactgctctgtaacatctcagagagggcccaagtctgagagtgagagtgagagtgagag 960
 QY 961 ctgagcacaactctgctgagcagaagagagcacaagaatctcctgagatctgcaagcaatctg 1020
 Db 961 ctgagcacaactctgctgagcagaagagagcacaagaatctcctgagatctgcaagcaatctg 1020

QY 1021 aacgatgccattaa 1035
 Db 1021 aacgatgccattaa 1035

RESULT 10

ID AAF72850
 ID AAF72850 standard; DNA; 1035 BP.

AC AAF72850;

DT 24-APR-2001 (first entry)

DE PGGB from spleen.

KM Heme biosynthetic pathway; gene therapy; AIP; ALA;

KM delta-aminolevulinic acid; deficient porphyria; ADP;

KM porphyria cutanea tarda; PCT; hereditary coproporphyrin; HCP;

KM congenital erythropoietic porphyria; VP;

KM erythropoietic protoporphyria; EPP;

KM hepatoerythropoietic porphyria; HEP; de.

OS Homo sapiens.

PN MO200107065-A2.

PD 01-FEB-2001.

PF 27-JUL-2000; 2000MO-DK00425.

PR 27-JUL-1999; 99DK-0001071.

PR 19-APR-2000; 2000DK-0000667.

PA (HEME-) HEMEBIOTECH AS.

PI Gellerfors P, Fogh J;

DR WPI; 2001-159639/16.

PT Treatment or prevention of porphyria, by enzyme replacement or gene

PT therapy for correction of mutations, particularly in the

PT porphobilinogen deaminase gene

PS Disclosure; Page 200-201; 207PP; English.

CC The present invention relates to treatment or prevention of a

CC disease caused by deficiency of at least one enzyme of the

CC heme biosynthetic pathway by administering at least one catalyst,

CC optionally combined with gene therapy of the relevant mutation,

CC The invention is useful for treating and/or preventing AIP, ALA

CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria

CC cutanea tarda (PCT), hereditary coproporphyrin (HCP), hereditary

CC (HCP), variegate porphyria (VP), congenital erythropoietic porphyria

CC (CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic

CC porphyria (HEP).

Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;

Query Match 99.8%; Score 1033.4; DB 22; Length 1035;
 Best Local Similarity 99.9%; Pred. No. 5,7e-279;
 Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atgagagtgatcgcgtggtgtaaccgcaagagccagcttgcgcatacagccgacagt 60
 Db 1 atgagagtgatcgcgtggtgtaaccgcaagagccagcttgcgcatacagccgacagt 60
 QY 61 gtgtgtgcaacattgaaagccctcgtaaccctgctgacgtttgaatcatctgtatgtcc 120
 Db 61 gtgtgtgcaacattgaaagccctcgtaaccctgctgacgtttgaatcatctgtatgtcc 120

QY	121	aaccaacgagagcaagattcttgaatactgacatctaaagatttgaaagaaagccgtttc	180
Db	121	aaccacagagagaaagaattcttgataactgcacccctcaagaatactgaaagaaagccgtttc	180
QY	181	aaccaagagactctgaaacatactgcctctgagaaagaaatgaaagtgaacctgtgttcaacctctg	240
Db	181	accaaaagagactctgaaacatactgcctctgagaaagaaatgaaagtgaacctgtgttcaacctctg	240
QY	241	aagagaaactgagccactgtgctctccctctgagcttcaacatcagaaagcattctgcaagcgggaa	300
Db	241	aagagaaactgagccactgtgctctccctctgagcttcaacatcagaaagcattctgcaagcgggaa	300
QY	301	aaacccctcaatgaaatgtctgtcttctcaaccccaaaattctgttgaaagaaacctgaagaaacctg	360
Db	301	aaacccctcaatgaaatgtctgtcttctcaaccccaaaattctgttgaaagaaacctgaagaaacctg	360
QY	361	ccagaggaagagatgtgtgtgtgtggaacaaacatccctccgcgaaagaaagacagccagctgcagaggaag	420
Db	361	ccagaggaagagatgtgtgtgtgtggaacaaacatccctccgcgaaagaaagacagccagctgcagaggaag	420
QY	421	ctcccgagacatcctgagagatctcaagagaaatctcgagggaagaaaccccaacaaacccgagctctcgaaagctg	480
Db	421	ctcccgagacatcctgagagatctcaagagaaatctcgagggaagaaaccccaacaaacccgagctctcgaaagctg	480
QY	481	gaagagagacagagagatctcaatctgacatccctcgagaaagaaagcttgagccctgcagagagcagatgggc	540
Db	481	gaagagagacagagagatctcaatctgacatccctcgagaaagaaagcttgagccctgcagagagcagatgggc	540
QY	541	tggacaaacccgggtcttgagcagatccctgcaccccttgagagaaatgaaatgaaatgaaatgaaatgaaatg	600
Db	541	tggacaaacccgggtcttgagcagatccctgcaccccttgagagaaatgaaatgaaatgaaatgaaatgaaatg	600
QY	601	ggggcccttgagagctgagaaagctgagacaaagacaaagacaaagacaaagacaaagacaaagacaaagac	660
Db	601	ggggcccttgagagctgagaaagctgagacaaagacaaagacaaagacaaagacaaagacaaagacaaagac	660
QY	661	ctgacagatcccgagactctgcttcgcctgacatcgactgaaagagcccttcctcaagagacactg	720
Db	661	ctgacagatcccgagactctgcttcgcctgacatcgactgaaagagcccttcctcaagagacactg	720
QY	721	gaagagagagctgagagctgagccagctgagccagctgagccagctgagccagctgagccagctgagccagctg	780
Db	721	gaagagagagctgagagctgagccagctgagccagctgagccagctgagccagctgagccagctgagccagctg	780
QY	781	ctgacatgagagagctctgagagctcaagagctcaagagctcaagagctcaagagctcaagagctcaagagct	840
Db	781	ctgacatgagagagctctgagagctcaagagctcaagagctcaagagctcaagagctcaagagctcaagagct	840
QY	841	aaccatcatgcttcctgc	900
Db	841	aaccatcatgcttcctgc	900
QY	901	atcatctgctgtgaaacatctcaacagagagcccccgtctgagctgagccagaaacttgagccatcagc	960
Db	901	atcatctgctgtgaaacatctcaacagagagcccccgtctgagctgagccagaaacttgagccatcagc	960
QY	961	ctggcccaaaactgtgtctgagagaaagagagccaaaaacaccccgagctgtgcaagagcagatg	1020
Db	961	ctggcccaaaactgtgtctgagagaaagagagccaaaaacaccccgagctgtgcaagagcagatg	1020
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Db	1021	aacgagatgccattaa	1035
RESULT 11			
AAAF72851			
ID AAF72851 standard: DNA: 1035 BP.			
AAAF72851:			
24-APR-2001 (first entry)			

DE	POGB from bone marrow #1.
XX	Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW	delta-aminolevulinic acid; deficient porphyria; ADP;
KW	porphyria cutanea tarda; PCT; hereditary coproporphyria; HCP;
KW	harderoporphyria; HDP; Variegata porphyria; VP;
KW	congenital erythropoietic porphyria; CEP;
KW	erythropoietic protoporphyria; EPP;
KW	hepatocrythropoietic porphyria; HEP; ds.
XX	
OS	Homo sapiens.
XX	
PN	MO200107065-A2.
XX	
PD	01-FEB-2001.
XX	
PF	27-JUL-2000; 2000MO-DK00425.
XX	
PR	27-JUL-1999; 99DK-0001071.
XX	
PA	19-APR-2000; 2000DK-0000667.
XX	
PI	(HEME-) HEMEBIOTECH AS.
XX	
DR	Gellerfors P, Fogh J;
XX	WPI: 2001-159639/16.
PT	Treatment or prevention of porphyria, by enzyme replacement or gene
XX	therapy for correction of mutations, particularly in the
XX	porphobilinogen deaminase gene
PS	Disclosure; Page 201; 207pp; English.
XX	
CC	The present invention relates to treatment or prevention of a
CC	disease caused by deficiency of at least one enzyme of the
CC	heme biosynthetic pathway by administering at least one catalyst,
CC	optionally combined with gene therapy of the relevant mutation.
CC	The invention is useful for treating and/or preventing AIP, ALA
CC	(delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC	cutanea tarda (PCT), hereditary coproporphyrin (HCP), harderoporphyria
CC	(HDP), variegata porphyria (VP), congenital erythropoietic porphyria
CC	(CEP), erythropoietic protoporphyria (EPP) and heptatoerythropoietic
CC	porphyria (HEP).
XX	
SQ	Sequence 1035 BP; 250 A; 271 C; 303 G; 211 T; 0 other;
	Query Match .99, 8%; Score 1033.4; DB 22; Length 1035;
	Best Local Similarity 99.9%; Pred. No. 5.7e-279;
	Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 atgagatgatctcgctgggtacccgcgaagaagcagcttctgcgatacagaagcaagt 60
DB	1 atgagaaatgattcgccttggtaccgccgaagaagcagcttctgcgatacagaagcaagt 60
QY	61 gtggctggcaaatctgaaaagccttcgtaacctgcgctcgctcgagtttgaaatcatgtctaagcc 120
DB	61 gtggctggcaaatctgaaaagccttcgtaacctgcgctcgctcgagtttgaaatcatgtctaagcc 120
QY	121 acccaagggaacaagaattcttatctgaactcttaagatctgaaagaaaacctgatt 180
DB	121 acccaagggaacaagaattcttgatactgaactcttaagatctgaaagaaaacctgatt 180
QY	181 accaagaagcttgaaacatgcccctbgagaagaatgaaagtgaacctggttgtctacacctg 240
DB	181 accaagaagcttgaaacatgcccctbgagaagaatgaaagtgaacctggttgtctacacctg 240
QY	241 aagaacctgcacatctgctctctctctctgcttcacacacggaagcaccatcgcaagcgagga 300
DB	241 aagaacctgcacatctgctctctctctctgcttcacacacggaagcaccatcgcaagcgagga 300
QY	301 aaacctatgatcgtgtgtcttccaaccaaaattgtttggaagaaaccttagaacctg 360
DB	301 aaacctatgatcgtgtgtcttccaaccaaaattgtttggaagaaaccttagaacctg 360

Db 301 aaccctcagtcgtctgtcttccaccnaaatgtgttggaagaccctagaaacctcg 360
 Qy 361 ccagagagaagtgctgttggaacacgctccctcggaagaagaccacgctgcagagaag 420
 Db 361 ccagagagaagtgctgttggaacacgctccctcggaagaagaccacgctgcagagaag 420
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 Db 421 tcccgacatctgagatctcagagatctcggagaaaccccaacacgctctcgaaagctg 480
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 Db 721 gaaagagagctgcagctgcagctgacagctgacagctatgaaagagatggagacatgac 780
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 Db 781 ctgacactggagagctgtgagatctagaagctcagatagatgacataagaagacatgacagct 840
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 Db 841 aacatcatgctcctcgtccacagatgaaagatggcctgtagagatgacacacagctgtgaaagc 900
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 Qy 961 ctgggcaactgtgtctgagacaaagggcccaaaaacatctcgtgagctgcacggcaatg 1020
 Db 961 ctgggcaactgtgtctgagacaaagggcccaaaaacatctcgtgagctgcacggcaatg 1020
 Qy 1021 aacgatatccattaa 1035
 Db 1021 aacgatatccattaa 1035
 RESULT 12
 AAX87636
 ID AAX87636 standard; cDNA: 1035 BP.
 AC AAX87636;
 DT 26-OCT-1999 (first entry)
 DE Human porphobilinogen deaminase clone 3.3.
 KW Porphobilinogen deaminase; human; haem; ALA deficiency porphyria;
 KW porphyria cutanea tarda; hereditary coproporphyria;
 KW harteoporphyria; congenital erythropoietic porphyria;
 KW variegate porphyria; erythropoietic protoporphyria;
 KW hepatoerythropoietic porphyria; acute intermittent porphyria;
 KW gene therapy; enzyme replacement therapy; db.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT variation replace(513..A)
 FT /*tag- a

FT /note- "silent mutation"
 FT replace(555..A)
 FT /*tag- b
 FT /note- "silent mutation"
 FT replace(729..C)
 FT /*tag- c
 FT /note- "silent mutation"
 FT replace(995..C)
 FT /*tag- d
 FT /note- "Asn to Thr substitution"
 FT replace(1017..G)
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 FT replace(1018..C)
 FT /*tag- f
 FT /note- "silent mutation"
 FT replace(1020..T)
 FT /*tag- g
 FT /note- "silent mutation"
 MO9317325-A2.
 PN 29-JUL-1999.
 PD 27-JAN-1999; 99MO-DK00040.
 PR 30-DEC-1998; 98DK-0001748.
 PR 27-JAN-1998; 98DK-0000112.
 XX
 PA (HEMB-) HEMEBIOTECH AS.
 PI Fogh J, Gellerfors P.
 PI
 DR MPI: 1999-476987/40.
 XX
 PT Treatment of acute intermittent porphyria and other porphyric
 PT diseases using an enzyme belonging to the haem biosynthetic pathway
 PS Disclosure: Page 94; 100pp; English.
 XX
 CC This is the nucleotide sequence of human PBGD clone 3.3 coding for
 CC an erythropoietic expressed form of porphobilinogen deaminase (PBGD).
 CC This enzyme catalyses the third, rate-limiting step of the haem
 CC biosynthetic pathway. PBGD was cloned from spleen, bone marrow,
 CC lymph node, lung, whole brain and adipose tissue cDNA using a
 CC nested PCR strategy. 8 PBGD clones were sequenced (see AAX87630 and
 CC AAX87632-38). Clone 3.3, from lymph node cDNA, has 6 changes from the
 CC previously published sequence. Clone 1.1 (see AAX87630) represents
 CC the most prevalent 'wild-type' allele in the population. Mutation
 CC of the PBGD gene is associated with the autosomal dominant disorder
 CC acute intermittent porphyria (AIP). A claimed method of treating a
 CC patient having a mutation in the PBGD gene comprises using a human
 CC PBGD cDNA sequence of either non-erythropoietic form (see AAX87631)
 CC or erythropoietic form (especially clone 1.1 cDNA), according
 CC to the tissue in which PBGD should be expressed, and transfection
 CC of the patient with the relevant cDNA. Gene therapy treatment of
 CC patients with AIP by a correction of one of the specific point
 CC mutations identified as causing the disease by use of chimera-plasty
 CC gene repair is also claimed. Other enzymes involved in the haem
 CC biosynthetic pathway can also be used to treat various porphyrias.
 CC
 SO Sequence 1035 BP; 250 A; 270 C; 303 G; 212 T; 0 other;
 Query Match 99.7%; Score 1031.8; DB 20; Length 1035;
 Best Local Similarity 99.8%; Pred. No. 1.6e-278;
 Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 atgagagtgatctgctgggttacccggaagacgagctgctgcatcagaagacagcagt 60
 Db 1 atgagagtgatctgctgggttacccggaagacgagctgctgcatcagaagacagcagt 60
 Qy 61 gtgtgtgcaacatgaaagcctctgacccctgagctgcagttgtaaatcatgtctatgtcc 120

[illegible]

XX	24-APR-2001 (first entry)	
DT		
DE	PDGB from lymph node #2.	
XX		
KW	Heme biosynthetic pathway; gene therapy; AIP; ALA;	
KW	delta-aminolevulinic acid; deficient porphyria; ADP;	
KW	porphyria cutanea tarda; PCT; hereditary coproporphyrin; HCP;	
KW	harderoporphyria; HDP; variegate porphyria; VP;	
KW	congenital erythropoietic porphyria; CEP;	
KW	erythropoietic protoporphyria; EPP;	
KW	hepatoerythropoietic porphyria; HEP; ds.	
XX		
OS	Homo sapiens.	
PN	MO200107065-A2.	
PD	01-FEB-2001.	
XX		
XX	27-JUL-2000; 2000WO-DK00435.	
PF		
XX	27-JUL-1999; 99DK-0001071.	
PR	19-APR-2000; 2000DK-0000667.	
XX		
PA	(HEME-) HEMEBIOTECH AS.	
XX		
P1	Gellerfors P, Fogh J;	
XX		
DR	WPI: 2001-159639/16.	
XX		
PT	Treatment or prevention of porphyria, by enzyme replacement or gene	
PT	therapy for correction of mutations, particularly in the	
PT	porphobilinogen deaminase gene	
XX		
XX		
PS	Disclosure; Page 202; 207pp; English.	
XX		
CC	The present invention relates to treatment or prevention of a	
CC	disease caused by deficiency of at least one enzyme of the	
CC	heme biosynthetic pathway by administering at least one catalyst,	
CC	optionally combined with gene therapy of the relevant mutation.	
CC	The invention is useful for treating and/or preventing AIP, ALA	
CC	(delta-aminolevulinic acid) deficient porphyria (ADP), porphyria	
CC	cutanea tarda (PCT), hereditary coproporphyrin (HCP), harderoporphyria	
CC	(HDP), variegate porphyria (VP), congenital erythropoietic porphyria	
CC	(CEP), erythropoietic protoporphyria (EPP) and hepatoerythropoietic	
CC	porphyria (HEP).	
XX		
XX		
SQ	Sequence 1035 BP; 250 A; 270 C; 303 G; 212 T; 0 other:	
	Query Match 99.7%; Score 1031.8; DB 22; Length 1035;	
	Best Local Similarity 99.8%; Pred. No. 1,6e-278;	
	Matches 1033; Conservative 0; Mismatches 2; Indels 0; Gaps	
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QY	121 acccaaggagacaagaattcttgatatactgcatactcttaagattgagagaaaaagctgttt 180	
DB	121 acccaaggagacaagaattcttgatatactgcatactctcttaagattgagagaaaaagctgttt 180	
QY	181 accaaggagactgtaaatagcctctgtagaagaagaatgtagcctgtgttgcatactcttg 240	
DB	181 accaaggagactgtaaatagcctctgtagaagaagaatgtagcctgtgttgcatactcttg 240	
QY	241 aagagacctgcacacttgcttccctccttgcttccacacatcgagacatctgcgaacgaggaa 3000	
DB	241 aagagacctgcacacttgcttccctccttgcttccacacatcgagacatctgcgaacgaggaa 3000	


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Db 61 gtgtgtgcaacattgaaagccctgcgtacccctgcctgcctgcttgaataatcattgtcattcc 120
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Db 121 accacaggggacaagaattccttgaactcactccttaagattgagagaaaaagcctgtt 180
Oy 181 accaagagcttgaacatgcccctggagaaagaatgaagtgagccctggttgcattcctctg 240
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Db 301 aacctcatgtctgttctcttccccaatttgttgggaagacccttagaaccttg 360
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RESULT 15
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AC AAF72856;
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DT 24-APR-2001 (first entry)
XX
DE PDB from total brain #2.
XX
KW Heme biosynthetic pathway; gene therapy; AIP; ALA;
KW delta-aminolevulinic acid; deficient porphyria; ADP;
KW porphyria cutanea tarda; PCP; hereditary coproporphyrin; HCP;
KW hereditary erythroid protoporphyria; HEP;
KW congenital erythropoietic porphyria; CEP;
KW erythropoietic protoporphyria; EPP;
KW hepatocellular porphyria; HEP; ds.
XX
OS Homo sapiens.
XX
PN M0200107065-A2.
XX
PD 01-FEB-2001.
XX
PF 27-JUL-2000; 2000MO-DK00425.
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PR 27-JUL-1999; 99DK-0001071.
XX
PR 19-APR-2000; 2000DK-0000667.
XX
PA (HEME-) HEMEBIOTECH AS.
XX
BI Gellerfors P., Fogh J.
XX
DR WPI: 2001-159639/16.
XX
PT Treatment or prevention of porphyria, by enzyme replacement or gene
PT therapy for correction of mutations, particularly in the
PT porphobilinogen deaminase gene -
XX
PS Disclosure: Page 203: 207pp: English.
XX
CC The present invention relates to treatment or prevention of a
CC disease caused by deficiency of at least one enzyme of the
CC heme biosynthetic pathway by administering at least one catalyst,
CC optionally combined with gene therapy of the relevant mutation.
CC The invention is useful for treating and/or preventing AIP, ALA
CC (delta-aminolevulinic acid) deficient porphyria (ADP), porphyria
CC cutanea tarda (PCP), hereditary coproporphyrin (HCP), hereditary
CC (HBP), variegata porphyria (VP), congenital erythropoietic porphyria
CC (CEP), erythropoietic protoporphyria (EPP) and hepatocellular
CC porphyria (HEP).
XX
SQ Sequence 1035 BP; 251 A; 272 C; 302 G; 210 T; 0 other;
Query Match 99.5%; Score 1030.2; DB 22; Length 1035;
Best Local Similarity 99.7%; Pred. No. 4,5e-278;
Matches 1032; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Search completed: October 6, 2001, 17:42:58
Job time: 305 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2001, 18:32:02 ; Search time 2932.86 Seconds
(without alignments)
5869.903 Million cell updates/sec

Title: US-09-601-138-12

Perfect score: 1113

Sequence: 1 cacacagccacttcccaag.....aattgacgacgcccattaa 1113

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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93: gb_pr9:*
94: gb_r01:*
95: gb_r02:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1113	100.0	1113	9	AX020193
2	1113	100.0	1113	10	AX079028
3	1106.6	99.4	1545	91	BC000520
4	1103.4	99.1	1377	93	HSPBGR2
5	1046	94.0	1380	93	HSPBGR
6	1035	93.0	1035	9	AX020182
7	1035	93.0	1035	10	AX079027
8	1035	93.0	1260	9	AX020191

9	1035	93.0	1260	10	AX079037	AX079037	Sequence
c 10	1035	93.0	3988	9	AX020180	AX020190	Sequence
c 11	1035	93.0	3988	10	AX079036	AX079036	Sequence
12	1033.4	92.8	1035	9	AX020184	AX020183	Sequence
c 13	1033.4	92.8	1035	9	AX020184	AX020184	Sequence
c 14	1033.4	92.8	1035	10	AX079029	AX079029	Sequence
15	1033.4	92.8	1035	10	AX079030	AX079030	Sequence
16	1032.6	92.8	5445	9	AX020182	AX020197	Sequence
17	1032.6	92.8	5445	10	AX079025	AX079025	Sequence
18	1031.8	92.7	1035	9	AX020187	AX020187	Sequence
19	1031.8	92.7	1035	10	AX079033	AX079033	Sequence
20	1030.2	92.6	1035	9	AX020189	AX079033	Sequence
21	1030.2	92.6	1035	10	AX079035	AX079035	Sequence
22	1028.6	92.4	1035	9	AX020186	AX079035	Sequence
23	1028.6	92.4	1035	10	AX079032	AX079032	Sequence
24	1021.4	91.8	1034	9	AX020185	AX020185	Sequence
25	1021.4	91.8	1034	9	AX020188	AX020188	Sequence
26	1021.4	91.8	1034	10	AX079031	AX079031	Sequence
27	1021.4	91.8	1034	10	AX079034	AX079034	Sequence
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29	862	77.4	1066	95	RSPHEMC	Rattus sp.	121006
30	833.2	74.9	1412	95	RNMBD	Rattus sp.	121006
31	797.3	71.7	1487	89	AX000628	Hom sapi	AX000628
32	236.2	21.2	123349	2	D90908	D90908	Synchocyst
c 33	176.8	15.9	9958	1	AE004938	AE004938	Pseudomon
34	177.6	15.6	6301	1	AF064061	AF064061	Pseudomon
35	172.2	15.5	10024	97	H0MPBD8A	H0MPBD8A	Hom sapi
36	172.2	15.5	122459	84	HSAC000384	HSAC000384	Hom sapi
c 37	172.2	15.5	144794	82	AP001182	AP001182	Hom sapi
c 38	172.2	15.5	157405	82	AP001315	AP001315	Hom sapi
c 39	172.2	15.5	190762	82	AP000833	AP000833	Hom sapi
c 40	172.2	15.5	196511	82	AP000854	AP000854	Hom sapi
c 41	163.4	14.6	294250	2	AP001517	AP001517	Bacillus
42	162	14.6	110000	84	MF6ICHR32_24	MF6ICHR32_24	Confination (25)
43	161	14.5	5852	2	AF221100	AF221100	Selenomon
44	160.6	14.4	26923	2	AX067466	AX067466	Sequence
45	159	14.3	1872	3	PSREKMD	PSREKMD	Pseudomonas

AA0709037 Sequence
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AA0709036 Sequence
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AA0709035 Sequence
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AA020188 Sequence
AA0709031 Sequence
AA0709034 Sequence
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Y12006 Rattus sp.
X06827 Rat (PBG-D)
AF0006628 Homo sapi
D90908 Synchocyst
AE004338 Pseudomon
AF064061 Pseudoba
MS56563 Homo sapie
AC0500368 Homo sap
AF0011182 Homo sap
AF0011181 Homo sap
AF0000853 Homo sap
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AP005157 Bacillus
Contribution (25
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AF054466 Sequence
W78444 Pseudomonas

ALIGNMENTS

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OY	1021	caaaacttgggatacagaagcttggccaactgtgtgtcgtgagcaaaaggaagccaaaacatccgt	1080
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ACCESSION	AX079028	Sequence	4 from Patent WO0107065.			
VERSION	AX079028.1	GI:13158603				
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ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE		1 (bases 1 to 1113)				
JOURNAL		Gellerfors, P. and Fogh, J.				
FEATURES		Production of rhbpgd and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyric diseases				
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VERSION	BC000520.1 GI:12653496		
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SOURCE	human.		
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 1545)		
JOURNAL	Strausberg,R. Direct Submission Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov		
COMMENT	Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: DCRD/DRP CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNI) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ nisc_mgc@nih.gov Contact: nisc_mgc@nih.gov Shaykhenko,Y., Weltherby,K.D., Beckstrom-Sternberg,S.M., Benjamin,B., Blakeley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S. Diatchin,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R. Lim,M., Maduro,Q.L., Mastello,C., Martinian,S.D., McLoskey,J.C., McOweil,J.J., Pearson,R., Snyder,B., Stantrippop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.		

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://Image.lnl.gov>
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 DEFINITION (hydroxymethylbilane synthase; EC4.3.1.8).
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 VERSION KERNOWS
 KEYWORDS hydroxymethylbilane synthase; porphobilinogen deaminase.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1377)
 AUTHORS Grandchamp, B., De Verneuil, H., Beaumont, C., Chretien, S., Walter, O.
 and Nordmann, Y.
 TITLE Tissue-specific expression of porphobilinogen deaminase. Two
 JOURNAL isoenzymes from a single gene
 MEDLINE Eur. J. Biochem. 162 (1), 105-110 (1987)
 COMMENT 87133520
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 ACCESSION X04217.1 GI:35306
 VERSION deaminase; porphobilinogen deaminase.
 KEYWORDS human.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1380)
 AUTHORS Raich,N., Romeo,P.H., Dubart,A., Beaupain,D., Cohen-Solal,M. and Goossens,M.

TITLE Molecular cloning and complete primary sequence of human erythrocyte porphobilinogen deaminase
 Nucleic Acids Res. 14 (15), 5955-5968 (1986)
 MEDLINE 86312872

COMMENT Porphobilinogen deaminase is the third enzyme of the heme biosynthetic pathway. Deficiency of this enzyme leads to the dominant hereditary disease Acute Intermittent Porphyrria (AIP).

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OY 1039 ctggccaactctgtctgctgagcaagagccaaaactccctggatgtctgacagggcaatg 1098
Db 961 CTGGCCAACTGTGCTGCTGCAAGAGGCCAAAACATCTGATGTTGCAACGCAATGTC 1020
OY 1099 aacgatgcccataa 1113
Db 1021 AACGATGCCCATTTAA 1035

RESULT 7
AX079027 AX079027 1035 bp DNA PAT 22-FEB-2001
LOCUS Sequence 3 from Patent WO0107065.
DEFINITION AX079027
ACCESSION AX079027
VERSION AX079027.1 GI:13158602
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1035)
AUTHORS Gellerfors, P. and Fogh, J.
TITILE Production of rhpbgd and new therapeutic methods for treating
patients with acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 0107065-A 3 01-FEB-2001;
Hembiotech A/S (DK)
FEATURES
Location/Qualifiers
source 1..1035
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 250 a 271 c 302 g 212 t
ORIGIN
Query Match 93.0%; Score 1035; DB 10; Length 1035;
Best Local Similarity 100.0%; Pred. No. 1,7e-237;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 379 aacctcctatgactgctgtctcttcaaccacaaattgttggagaagaccctcagaaccctg 438
Db 301 AACCTCATGATGCTGTTGTTTACCCAAAATTTGTTGGAGAACCCCTAGAAACCTTG 360
OY 439 ccagagaagagctgtgtaggaacacagctccctggcgaagaagacccagctgagagaagag 498
Db 361 CCAGAGAAAGTGTGTGGGAAACAGCTCCCTGCAAGAGAGCCAGCTGCAAGAGAAAG 420
OY 499 tcccgatctgagctcagaagatattcggggaaacctcaacacccagctctggagaactg 558
Db 421 TTCCCGCATCTGGAGTTCAGAGATATTCGGGGAAACCTCAACACCCGCTTCGGAAGCTG 480
OY 559 gacgaagcagagagttcagtgccatcactccctggagaagaagctggccagagcagagggc 618
Db 481 GACGAGCAGAGAGAGTTCCAGTCCATCATCTGAGCAAGAGCTGGCCATGAGCGATGGGC 540
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OY 1099 aacgatgcccataa 1113
Db 1021 AACGATGCCCATTTAA 1035

RESULT 8
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LOCUS Sequence 10 from Patent WO937325.
DEFINITION AX020191
ACCESSION AX020191
VERSION AX020191.1 GI:10043982
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Fogh, J. and Gellerfors, P.
TITILE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 937325-A 10 29-JUL-1993;
FOGH JENS (DK); HEMBIOTECH A S (DK); GELLERFORS PAER (SE)
FEATURES
Location/Qualifiers
source 1..1260
/organism="unidentified"

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BASE COUNT 309 a /db_xref="taxon:32644" 258 t
 ORIGIN 335 c 358 g

Query Match 93.0%; Score 1035; DB 9; Length 1260;
 Best Local Similarity 100.0%; Pred. No. 1.6e-237;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 199 accacagggagacagatctctgtatctactctcctaagatttgagagaaagccgttt 258
 DB 251 ACCACAGGGAGACAGATTCTGTATCTGCATCTTAAGATTGAGAGAGAAACCTGTTT 310
 QY 259 accaaggaagcttgaaacatgacctgagagaaatgaagtgagacctggttctcaactctgt 318
 DB 311 ACCAAGGAGCTTGAACTGCTGAGAGAAATGAACTGACCTGCTGTCTCACTCTTG 370
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 DB 371 AAGGACCTGCCACAGCTGCTCTCTCTGCTTCAACATCGAGCCATCTGCAAGCCGGAA 430
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 DB 431 AACCTCATGATGCTGTGTTCTTTCACCCAAATTTTGTGGAGAACCTGAGAACCTTG 490
 QY 439 ccagagaaagtggtgtgagacacagctccctcgtcgaagacacacacagctgacagaaag 498
 DB 491 CCAGAAAGAGTGTGTGGAGAACACAGCTCCCTGGAAGACAGCCAGCTGCGAGAAAG 550
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 QY 1099 aacgatgccatcaa 1113
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RESULT 9

AX079037 1260 bp DNA PAT 22-FEB-2001
 LOCUS
 DEFINITION Sequence 13 from Patent WO0107065.
 AX079037
 VERSION AX079037
 KEYWORDS GI:13158612

SOURCE

human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 1260)
 Gellerfors, P. and Fogh, J.
 Production of ribbed and new therapeutic methods for treating
 patients with acute intermittent porphyria (aip) and other
 porphyric diseases
 Patent: WO 0107065-A 13 01-FEB-2001;

JOURNAL

Hemebiotech A/S (DK)

FEATURES

source

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/organism="Homo sapiens"

/db_xref="taxon:9606"

BASE COUNT 309 a 335 c 358 g 258 t

ORIGIN

Query Match 93.0%; Score 1035; DB 10; Length 1260;
 Best Local Similarity 100.0%; Pred. No. 1.6e-237;
 Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 atgagagtcgtcgtggtgtaaccgcaagagccagctgtctcgaacagagcagc 138
 DB 131 ATGAGAGTATGCGGTGGGTACCCGCAAGAGCCAGCTGCTCCATACAGAGCGACGT 190
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 DB 371 AAGGACCTGCCACAGCTGCTCTCTCTGCTTCAACATCGAGCCATCTGCAAGCGGAA 430
 QY 379 aaccctcagatgctgtgtgtcttccacccaatttcttgagagagaccctagaacctgt 438
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Dh 611 GACGACGACGAGAGTTCAGTCCATFATCTCGGACAGAGCTGGCTCCGACGCCATGGC 670
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RESULT 10
AX020190/c 3988 bp DNA PAT 07-SEP-2000
LOCUS AX020190 Sequence 9 from Patent WO9937325.
DEFINITION AX020190
ACCESSION AX020190.1 GI:10043981
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3988)
AUTHORS Fogh,J. and Gellerfors,P.
TITLE Method for treating acute intermittent porphyria (aip) and other porphyric diseases
PATENT: WO 9937325-A 9 29-JUL-1999;
JOURNAL PUGH JEMS (DK); HEMBIOTEC A S (DK); GELLERFORS PABR (SE)
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source location/Qualifiers
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Query Match 93.0%; Score 1035; DB 9; Length 3988;
Best local similarity 100.0%; Pred. No. 1,4e-237;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 139 gttgtgtgaacattgaaagcctgtaacctcgtgacctgagattgaaatattgtctatgcc 198
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Dh 1670 GTGGTGCAACATTGAAAGCCTCGTACCTGGCTGCAGTTTGAAATCATTTGCTATGTCC 1611
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Qy 379 aacctatgattctgttcttcaacaaaatttgttggagagaccctagaagaaacctg 438
Dh 1430 AACCTATATATCTCTTGTCTTCAACCCAAATTTGTTGGAAAGACCTTAGAACCCTG 1371
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Dh 1370 CCAGAGAAAGATGTGTGGGAAACAGCTCCTGCGAAGACGCCAGCTGCAGAGAAAG 1311
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RESULT 11
AX079036/c 3988 bp DNA PAT 22-FEB-2001
LOCUS AX079036 Sequence 12 from Patent WO0107065.
DEFINITION AX079036
ACCESSION AX079036.1 GI:13158611
VERSION

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS 1 (bases 1 to 3988)
TITLE Gellierfors, P. and Fogh, J.
JOURNAL Production of rhpbgd and new therapeutic methods for treating patients with acute intermittent porphyria (aip) and other porphyric diseases
Patient: MO 0107065-A 12 01-FEB-2001;
Hembiotech A/S (DK)
FEATURES
Location/Qualifiers
source 1..3988
BASE COUNT 918 a 1056 c 1000 g 1014 t
ORIGIN

Query Match 93.0%; Score 1035; DB 10; Length 3988.
Best Local Similarity 100.0%; Pred. No. 1,4e-237;
Matches 1035; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 atgagagtgatcgcgctgggtaccgaagagcagcttgctgcatacagacgagcagt 138
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DB 1550 ACCAAGAGCTTGAACATGCCCTGAGAGAAATGAATGAACCTGCTGTGTTCACTCTTG 1491
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DB 710 AACGATGCCCATTTAA 696

RESULT 12
AX020183 1035 bp DNA PAT 07-SEP-2000
LOCUS Sequence 2 from Patent WO9937325.
DEFINITION AX020183
ACCESSION AX020183
VERSION AX020183.1 GI:10043974
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Fogh, J. and Gellierfors, P.
TITLE Method for treating acute intermittent porphyria (aip) and other porphyric diseases
JOURNAL Patent: WO 9937325-A 2 29-JUL-1999;
FOGH JENS (DK); HEMBIOTECH A S (DK); GELLIERFORS PAER (SE)
FEATURES
source 1..1035
Location/Qualifiers
BASE COUNT 250 a 271 c 303 g 211 t
ORIGIN

Query Match 92.8%; Score 1033.4; DB 9; Length 1035;
Best Local Similarity 99.9%; Pred. No. 4e-237;
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 259 accaagagcttgaaacatgcccctggaagaaatgaaatggaactgtgttcaactcctg 318
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DB 241 AAGGAACCTGCCACATGCTCTCTCTGCTTCAACATGCTGAGACCATCTGCAAGCGGAA 300
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Db 301 AACCTATATGCTGTGTTGCTTTTCACCCAAAATTGTTGGAGAACCTTGAAACCTTG 360
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Db 361 CCAAGAGAAGAGTGTGTGGGAAACACAGCTCCCTGCGAAGAGCAGCCACACTGCAAGAGAA 420
OY 499 ttcccgatctgtagtctgagagatctgaggaaccccaaaccccgcttcggaactg 558
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Db 421 TTCCCGATCTGGAGTTCCAGAGATATTGGGAAACCTCAACACCCGGCTTCGGAACCTG 480
OY 559 gacagagaagaagatctagctgacacacccgagcaagaagcttgagctgcaagcagatggc 618
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Db 781 CTGAGTGGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 840
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RESULT 13
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DEFINITION Sequence 3 from Patent WO9937325.
ACCESSION AX020184
VERSION AX020184.1 GI:10043975
KEYWORDS
SOURCE unidentifed.
ORGANISM unidentifed.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Fogh,J. and Gellerfors,P.
TITLE Method for treating acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 9937325-A 3 29-JUL-1999;
FOGH JENS (DK); HEHEBIOTCH A S (DK); GELLERFORS PAER (SE)
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location/Qualifiers
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BASE COUNT 250 a 271 c 303 g 211 t

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Query Match 92.8%; Score 1033.4; DB 9; Length 1035;
Best Local Similarity 99.9%; Pred. No. 4e-237;
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 79 atgagatgatttcgtgtggttacccgaaagacgcagcttgctgcatcacagaggaagat 138
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Db 241 AAGGACCTGCCACAGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
OY 379 aacctcatgactgtgtgtctctcaccacacacacacacacacacacacacacacac 438
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Db 301 AACCTCATGATGCTGTTGTCTTTCACCCAAAATTGTTGGAGAACCTTGAAACCTTG 360
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Db 361 CCAAGAGAGATGTGTGGGAGACCACTCTGCAAGAGCGCCACACTGCAAGAGAA 420
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Db 421 TTCCCGATCTGGAGTTCCAGAGATATTGGGAAACCTCAACACCCGGCTTCGGAACCTG 480
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Db 961 CTGCCAACTGTTGCTGAGCAAGAGCCAAAACATCTGATGTTGCAGCGCAATTG 1020
Oy 1099 bagatgccattaa 1113
Db 1021 AAGCATGCCCATTTAA 1035

RESULT 14
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LOCUS Sequence 5 from Patent WO0107065.
DEFINITION AX079029
ACCESSION AX079029
VERSION AX079029.1 GI:13158604
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Gellerfors, P. and Fogh, J.
TITLE Production of rhpbpd and new therapeutic methods for treating
patients with acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 0107065-A 5 01-FEB-2001;
Hemabiotech A/S (DK)
FEATURES
Source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 250 a 271 c 303 g 211 t
ORIGIN

Query Match 92.8%; Score 1033.4; DB 10; Length 1035;
Best Local Similarity 99.9%; Pred. No. 4e-237;
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 79 atagaagatgatcgatcgatgagatccgcgaagacagcttgctgcactacagaagagcagt 138
Db 1 ATGAGAGTATTCGGCTGGGTACCCGCAAGAGCCAGCTTGCTGCCTACAGAGGAGCACT 60
Oy 139 gtgtgtgcaacattgaaagcctcgtaaccctgctgagctgagcttgtaacatctgatactc 198
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Oy 199 accacaggggaagaagattcttgatatactgactctctaagaattggagaagaagccgttt 258
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Oy 439 ccagaagaagatgtgtgtggaagacagctccctcggaagaagacacacacacacacacacac 498
Db 361 CCAGAGAAGAGTGTGTGTGGGAACACAGCTCCCTCGGAAGAGACACCCAGCTCGAGAAAG 420
Oy 499 ttccgcgactctgagatctcaagagtaattccgaggaagaacctcaacacccggtctggaagctg 558
Db 421 TTCCCGCATCTGAGTTAGAGATTCGGGGAAACCTCAACACCCGCGCTTGGGAAGCTG 480
Oy 559 gacgagcagcaggaatcaagtgcatactctgcaacaacagctgagcctgcaagcgacatgggc 618
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Oy 1099 aacgatgccattaa 1113
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RESULT 15
AX079030 1035 bp DNA PAT 22-FEB-2001
LOCUS Sequence 6 from Patent WO0107065.
DEFINITION AX079030
ACCESSION AX079030
VERSION AX079030.1 GI:13158605
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1035)
AUTHORS Gellerfors, P. and Fogh, J.
TITLE Production of rhpbpd and new therapeutic methods for treating
patients with acute intermittent porphyria (aip) and other
porphyric diseases
JOURNAL Patent: WO 0107065-A 6 01-FEB-2001;
Hemabiotech A/S (DK)
FEATURES
Source Location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 250 a 271 c 303 g 211 t
ORIGIN

Query Match 92.8%; Score 1033.4; DB 10; Length 1035;
Best Local Similarity 99.9%; Pred. No. 4e-237;
Matches 1034; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 79 atagaagatgatcgatcgatgagatccgcgaagacagcttgctgcactacagaagagcagt 138
Db 1 ATGAGAGTATTCGGCTGGGTACCCGCAAGAGCCAGCTTGCTGCCTACAGAGGAGCACT 60
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